

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 28.6916 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-166
Perfect score: 30
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	30	100.0	30	17	AAR88832	Human parathyroid	
2	30	100.0	30	23	AAU73051	Parathyroid hormon	
3	30	100.0	31	19	AAW42059	Human parathyroid	
4	30	100.0	31	19	AAW42051	Human parathyroid	
5	30	100.0	31	20	AAV02578	N-terminal 31 resi	
6	30	100.0	31	22	AAB81080	Human parathyroid	
7	30	100.0	31	22	AAB91097	Parathyroid hormon	
8	30	100.0	31	23	AAE23720	Human parathyroid	
9	30	100.0	31	23	AAU73039	Parathyroid hormon	
10	30	100.0	31	23	AAU73177	Parathyroid hormon	
11	30	100.0	32	23	AAU73176	Parathyroid hormon	
12	30	100.0	33	21	AAV98018	Human amino-termin	
13	30	100.0	34	4	AAP30022	Human parathyroid-	
14	30	100.0	34	6	AAP50377	[Met(O)8,18]hPTH-(
15	30	100.0	34	7	AAP60031	Sequence of the fi	
16	30	100.0	34	11	AAR07919	Human parathyroid	
17	30	100.0	34	11	AAR07922	Human parathyroid	
18	30	100.0	34	13	AAR22283	Parathyroid hormon	
19	30	100.0	34	14	AAR41549	[D-Ser3]hPTH (1-34	
20	30	100.0	34	14	AAR41570	[Gln25]hPTH (1-34)	
21	30	100.0	34	15	AAR58291	[Lys(For)26, Lys(F	
22	30	100.0	34	15	AAR58228	[D-Asp30]-hPTH(1-3	
23	30	100.0	34	15	AAR58232	[Lys32]-hPTH(1-34)	
24	30	100.0	34	15	AAR58181	[Thr33, Ala34]-hPT	
25	30	100.0	34	15	AAR58016	N-alpha-Isopropyl-	
26	30	100.0	34	15	AAR58017	[Lys(N-epsilon-Iso	
27	30	100.0	34	15	AAR55724	Parathormone N-ter	
28	30	100.0	34	16	AAR74521	Human parathyroid	
29	30	100.0	34	17	AAW99449	Human parathyroid	
30	30	100.0	34	17	AAR99978	Human parathyroid	
31	30	100.0	34	17	AAR98951	Target peptide (PT	
32	30	100.0	34	17	AAR98966	PTH(1-34). Not sp	
33	30	100.0	34	17	AAR88835	Human parathyroid	
34	30	100.0	34	18	AAW24273	Wild type parathyr	
35	30	100.0	34	18	AAW19994	Cyclised human par	
36	30	100.0	34	18	AAW20000	Cyclised human par	
37	30	100.0	34	18	AAW20006	Cyclised human par	
38	30	100.0	34	18	AAW17948	Human parathyroid	
39	30	100.0	34	18	AAW17968	Human parathyroid	
40	30	100.0	34	18	AAW17955	Human parathyroid	
41	30	100.0	34	19	AAW67283	Parathyroid hormon	
42	30	100.0	34	19	AAW67291	Parathyroid hormon	
43	30	100.0	34	19	AAW61658	Parathyroid hormon	
44	30	100.0	34	19	AAW65975	Human parathyroid	
45	30	100.0	34	19	AAW42614	Human parathyroid	
46	30	100.0	34	19	AAW48392	Human parathyroid	
47	30	100.0	34	20	AAV50593	Resin bound cyclic	
48	30	100.0	34	20	AAV17752	Human parathyroid	
49	30	100.0	34	20	AAV14151	Human parathyroid	
50	30	100.0	34	20	AAV02579	N-terminal 34 resi	

51	30	100.0	34	20	AAW81871	Human PTH N-termin
52	30	100.0	34	21	ABJ10712	Human parathyroid
53	30	100.0	34	21	AAB07454	Amino acids 1-34 o
54	30	100.0	34	21	AAV98017	Human amino-termin
55	30	100.0	34	21	AAV82631	Human parathyroid
56	30	100.0	34	21	AAV68763	Amino acids 1-34 o
57	30	100.0	34	22	AAB84778	Native rat parathy
58	30	100.0	34	22	AAB96898	Human parathyroid
59	30	100.0	34	22	AAB96929	Human parathyroid
60	30	100.0	34	22	AAB81079	Human parathyroid
61	30	100.0	34	22	AAB91098	Parathyroid hormon
62	30	100.0	34	23	ABJ05328	Human PTH(1-34) pe
63	30	100.0	34	23	AAE23727	Human parathyroid
64	30	100.0	34	23	ABB06329	Human parathyroid
65	30	100.0	34	23	ABB08595	C-terminal truncat
66	30	100.0	34	23	AAE18395	Human PTH peptide
67	30	100.0	34	23	ABB07147	Parathyroid hormon
68	30	100.0	34	23	AAU73028	Parathyroid hormon
69	30	100.0	34	24	ABP71500	Human parathyroid
70	30	100.0	34	24	ABG74235	Human parathyroid
71	30	100.0	35	22	AAB91112	Parathyroid hormon
72	30	100.0	35	23	AAU73172	Parathyroid hormon
73	30	100.0	36	14	AAR39450	Ser-Val-(hPTH 3-35
74	30	100.0	36	15	AAR58286	[D-Leu24]-hPTH(1-3
75	30	100.0	36	15	AAR58292	[D-Lys27]-hPTH(1-3
76	30	100.0	36	15	AAR58293	[D-Leu28]-hPTH(1-3
77	30	100.0	36	15	AAR58294	[D-Phe34]-hPTH(1-3
78	30	100.0	36	15	AAR58295	[D-Val35]-hPTH(1-3
79	30	100.0	36	15	AAR58296	[Ala35]-hPTH(1-36)
80	30	100.0	36	15	AAR58297	[Pro35]-hPTH(1-36)
81	30	100.0	36	15	AAR58298	[NMeVal35]-hPTH(1-
82	30	100.0	36	15	AAR58299	[Thr35,Ala36]-hPTH
83	30	100.0	36	15	AAR58300	[D-Ala36]-hPTH(1-3
84	30	100.0	36	15	AAR58301	[NMeAla36]-hPTH(1-
85	30	100.0	36	15	AAR58260	[D-Val2]-hPTH(1-36
86	30	100.0	36	15	AAR58263	[D-Ile5]-hPTH(1-36
87	30	100.0	36	15	AAR58264	[D-Gln6]-hPTH(1-36
88	30	100.0	36	15	AAR58265	[D-Leu7]-hPTH(1-36
89	30	100.0	36	15	AAR58270	[D-Leu11]-hPTH(1-3
90	30	100.0	36	15	AAR58272	[D-Lys13]-hPTH(1-3
91	30	100.0	36	15	AAR58273	[D-Leu15]-hPTH(1-3
92	30	100.0	36	15	AAR58276	[Met(O2)18]-hPTH(1
93	30	100.0	36	15	AAR58278	[D-Met18]-hPTH(1-3
94	30	100.0	36	15	AAR58280	[D-Arg20]-hPTH(1-3
95	30	100.0	36	15	AAR58281	[D-Val21]-hPTH(1-3
96	30	100.0	36	15	AAR58284	[D-Trp23]-hPTH(1-3
97	30	100.0	36	15	AAR58227	[D-Gln29]-hPTH(1-3
98	30	100.0	36	15	AAR58230	[D-Val31]-hPTH(1-3
99	30	100.0	36	15	AAR58231	[Ala31]-hPTH(1-36)
100	30	100.0	36	15	AAR58233	[D-His32]-hPTH(1-3
101	30	100.0	36	15	AAR58234	[Ala32]-hPTH(1-36)
102	30	100.0	36	15	AAR58235	[D-Asn33]-hPTH(1-3
103	30	100.0	36	15	AAR58236	[Ala33]-hPTH(1-36)
104	30	100.0	36	15	AAR58237	[NMePhe34]-hPTH(1-
105	30	100.0	36	15	AAR58238	[D-Asp30]-hPTH(1-3
106	30	100.0	36	15	AAR58242	[Lys(Isopropyl)13]
107	30	100.0	36	15	AAR58246	Acetyl-hPTH(1-36)-

108	30	100.0	36	15	AAR58249	[D-Ser1]-hPTH(1-36
109	30	100.0	36	15	AAR58191	[Ala34]-hPTH(1-36)
110	30	100.0	36	15	AAR58196	[D-Phe34, D-Ala36]
111	30	100.0	36	15	AAR58198	[D-Ser3]-hPTH(1-36
112	30	100.0	36	15	AAR58199	[D-Glu4]-hPTH(1-36
113	30	100.0	36	15	AAR58200	[D-His9]-hPTH(1-36
114	30	100.0	36	15	AAR58202	[D-Asn10]-hPTH(1-3
115	30	100.0	36	15	AAR58210	[D-His14]-hPTH(1-3
116	30	100.0	36	15	AAR58211	[D-Asn16]-hPTH(1-3
117	30	100.0	36	15	AAR58213	[D-Ser17]-hPTH(1-3
118	30	100.0	36	15	AAR58215	[D-Glu19]-hPTH(1-3
119	30	100.0	36	15	AAR58220	[D-Lys26]-hPTH(1-3
120	30	100.0	36	15	AAR58171	[N-Me-Ser1]-hPTH(1
121	30	100.0	37	12	AAR11882	Parathyroid hormon
122	30	100.0	37	13	AAR24778	hPTH(1-37)-amide/e
123	30	100.0	37	15	AAR58244	[Ala0]-hPTH(1-36) -
124	30	100.0	37	15	AAR58245	[Pro0]-hPTH(1-36) -
125	30	100.0	37	22	AAB86226	Human parathyroid
126	30	100.0	37	22	AAB86229	Human parathyroid
127	30	100.0	37	23	ABB82203	Human parathyroid
128	30	100.0	38	3	AAP20248	Parathyroid hormon
129	30	100.0	38	15	AAR58282	[Trp(SO2Pmc)23]-hP
130	30	100.0	38	15	AAR58283	[Trp(Pmc)23]-hPTH(
131	30	100.0	38	15	AAR58018	Isopropyl-[Lys(Iso
132	30	100.0	38	15	AAR58162	[Arg33]-hPTH(1-38)
133	30	100.0	38	15	AAR58163	[Pro33]-hPTH(1-38)
134	30	100.0	38	15	AAR58164	[Asp33]-hPTH(1-38)
135	30	100.0	38	15	AAR58165	[Ile33]-hPTH(1-38)
136	30	100.0	38	15	AAR58166	[Lys33]-hPTH(1-38)
137	30	100.0	38	15	AAR58167	[Ile31,Arg33]-hPTH
138	30	100.0	38	15	AAR58075	[Ser33]-hPTH(1-38)
139	30	100.0	38	15	AAR58076	[Thr33]-hPTH(1-38)
140	30	100.0	38	15	AAR58077	[Leu33]-hPTH(1-38)
141	30	100.0	38	15	AAR58078	[Gly33]-hPTH(1-38)
142	30	100.0	38	15	AAR58084	[Gln33]-hPTH(1-38)
143	30	100.0	38	15	AAR54234	PTH N-terminal. S
144	30	100.0	38	20	AAU02580	N-terminal 38 resi
145	30	100.0	38	22	AAB91101	Parathyroid hormon
146	30	100.0	38	23	AAE23729	Human parathyroid
147	30	100.0	38	23	AAE18400	Human PTH peptide
148	30	100.0	38	23	AAU73026	Parathyroid hormon
149	29	96.7	29	17	AAR88836	Human parathyroid
150	29	96.7	29	23	AAU73063	Parathyroid hormon
151	29	96.7	30	23	AAU73055	Parathyroid hormon
152	29	96.7	30	23	AAU73178	Parathyroid hormon
153	29	96.7	33	21	AAU98012	Human amino-termin
154	29	96.7	33	21	AAU98015	Human amino-termin
155	29	96.7	34	21	AAU98010	Human amino-termin
156	29	96.7	34	21	AAU98011	Human amino-termin
157	29	96.7	34	21	AAU98014	Human amino-termin
158	29	96.7	34	22	AAB91113	Parathyroid hormon
159	29	96.7	34	23	AAE23728	Human parathyroid
160	29	96.7	34	23	AAE18399	Human PTH peptide
161	29	96.7	34	23	AAU73032	Parathyroid hormon
162	29	96.7	36	12	AAR15842	Human parathyroid
163	29	96.7	36	13	AAR23995	Human paprthyroid
164	29	96.7	36	15	AAR58254	[4-aminosalicylic

165	29	96.7	36	15	AAR58255	[TMSA1]-hPTH(1-36)
166	29	96.7	36	15	AAR58256	[Phe1]-hPTH(1-36)-
167	29	96.7	36	15	AAR58257	[Propargylglycin1]
168	29	96.7	36	15	AAR58262	[Ala1]-hPTH(1-36)-
169	29	96.7	36	15	AAR58229	[Ala30]-hPTH(1-36)
170	29	96.7	36	15	AAR58243	Propargyl-[Al]-hPT
171	29	96.7	36	15	AAR58247	[Hyp1]-hPTH(1-36)-
172	29	96.7	36	15	AAR58248	N-Dimethyl-[Ala1]-
173	29	96.7	36	15	AAR58250	[Lys(For)1]-hPTH(1
174	29	96.7	36	15	AAR58251	[D-glyceric acid1]
175	29	96.7	36	15	AAR58252	[Asn1]-hPTH(1-36)-
176	29	96.7	36	15	AAR58253	[4-aminobenzoic ac
177	29	96.7	36	15	AAR58169	[D-Prol]-hPTH(1-36
178	29	96.7	36	15	AAR58170	[Nva1]-hPTH(1-36)-
179	29	96.7	36	15	AAR58172	[Indole-2-carboxyl
180	29	96.7	36	15	AAR58173	[Indole-3-carboxyl
181	29	96.7	36	15	AAR58174	[Pyridine-3-carbox
182	29	96.7	36	15	AAR58175	[Pyridine-2-carbox
183	29	96.7	36	15	AAR58176	[Hexahydropyridazi
184	29	96.7	36	15	AAR58177	[Morpholine-2-carb
185	29	96.7	36	15	AAR58178	[Prol]-hPTH(1-36)-
186	29	96.7	36	15	AAR58179	[Leu1]-hPTH(1-36)-
187	29	96.7	36	15	AAR58180	[Ile1]-hPTH(1-36)-
188	29	96.7	36	15	AAR58026	N-alpha-methyl[Ala
189	29	96.7	36	15	AAR58168	[1-amino-cyclopent
190	29	96.7	37	23	AAU73027	Parathyroid hormon
191	29	96.7	38	15	AAR58019	N-alpha-methyl[Ala
192	29	96.7	38	15	AAR58022	[Ile1]-hPTH(1-38)-
193	29	96.7	38	15	AAR58028	[Thr1]-hPTH(1-38)-
194	29	96.7	38	15	AAR58029	[Leu1]-hPTH(1-38)-
195	29	96.7	38	15	AAR58030	[Abu1 or Gabal]-hP
196	28	93.3	28	17	AAR88837	Human parathyroid
197	28	93.3	28	21	AAU98052	Human parathyroid
198	28	93.3	28	23	AAU73064	Parathyroid hormon
199	28	93.3	29	12	AAR11731	Adenine-rich PTH-(
200	28	93.3	29	23	AAU73179	Parathyroid hormon
201	28	93.3	32	5	AAP40427	Parathyroid antago
202	28	93.3	34	18	AAW01610	Parathyroid hormon
203	28	93.3	34	19	AAW67293	Parathyroid hormon
204	28	93.3	34	22	AAB61638	Peptide #1 that ca
205	28	93.3	36	15	AAR58259	[aBU2]-hPTH(1-36)-
206	28	93.3	36	15	AAR58261	[Tert.Leu]-hPTH(1-
207	28	93.3	36	15	AAR58190	[Ala29]-hPTH(1-36)
208	28	93.3	38	15	AAR58023	[Ala1, Abu2 or Nva2
209	28	93.3	38	15	AAR58024	[Ala1, Ile2]-hPTH(1
210	27	90.0	28	21	AAU98048	Human parathyroid
211	27	90.0	28	21	AAU98050	Human parathyroid
212	27	90.0	31	5	AAP40760	Human parathyroid
213	27	90.0	34	14	AAR41550	[D-Ala3]hPTH (1-34
214	27	90.0	34	18	AAW17947	Human parathyroid
215	27	90.0	34	18	AAW17951	Human parathyroid
216	27	90.0	34	18	AAW17957	Human parathyroid
217	27	90.0	34	19	AAW67282	Parathyroid hormon
218	27	90.0	34	19	AAW67286	Parathyroid hormon
219	27	90.0	36	15	AAR58197	[Ala3]-hPTH(1-36)-
220	27	90.0	38	15	AAR58159	[Val28]-hPTH(1-38)
221	27	90.0	38	15	AAR58160	[Ile28]-hPTH(1-38)

222	27	90.0	38	15	AAR58161	[Pro3,Thr33]-hPTH(
223	26	86.7	28	17	AAR88838	Human parathyroid
224	26	86.7	28	22	AAB81074	Human parathyroid
225	26	86.7	29	17	AAR88839	Human parathyroid
226	26	86.7	29	22	AAB81075	Human parathyroid
227	26	86.7	30	17	AAR88833	Human parathyroid
228	26	86.7	30	19	AAW42052	Human parathyroid
229	26	86.7	30	23	AAE23752	Human parathyroid
230	26	86.7	30	23	AAU73062	Parathyroid hormon
231	26	86.7	31	19	AAW42056	Human parathyroid
232	26	86.7	31	19	AAW42057	Human parathyroid
233	26	86.7	31	19	AAW42060	Human parathyroid
234	26	86.7	31	19	AAW42062	Human parathyroid
235	26	86.7	31	19	AAW42067	Human parathyroid
236	26	86.7	31	19	AAW42049	Human parathyroid
237	26	86.7	31	19	AAW42050	Human parathyroid
238	26	86.7	31	19	AAW42053	Human parathyroid
239	26	86.7	31	23	AAU73040	Parathyroid hormon
240	26	86.7	31	23	AAU82640	Analogue of human
241	26	86.7	32	23	AAE23735	Human parathyroid
242	26	86.7	34	13	AAR22298	Human parathyroid
243	26	86.7	34	13	AAR22299	Human parathyroid
244	26	86.7	34	14	AAR41554	[Thr27]hPTH (1-34)
245	26	86.7	34	14	AAR41555	[Asn27]hPTH (1-34)
246	26	86.7	34	14	AAR41558	[Ser27]hPTH (1-34)
247	26	86.7	34	14	AAR41559	[Gly27]hPTH (1-34)
248	26	86.7	34	14	AAR41560	[His27]hPTH (1-34)
249	26	86.7	34	17	AAR88829	Human parathyroid
250	26	86.7	34	17	AAR88834	Human parathyroid
251	26	86.7	34	18	AAW17969	Human parathyroid
252	26	86.7	34	19	AAW67292	Parathyroid hormon
253	26	86.7	34	19	AAW67297	Parathyroid hormon
254	26	86.7	34	19	AAW42054	Human parathyroid
255	26	86.7	34	19	AAW42055	Human parathyroid
256	26	86.7	36	15	AAR58222	[His27]-hPTH(1-36)
257	26	86.7	36	15	AAR58223	[Phe27]-hPTH(1-36)
258	26	86.7	36	15	AAR58224	[Nle27]-hPTH(1-36)
259	26	86.7	36	15	AAR58225	[Asn27]-hPTH(1-36)
260	26	86.7	36	15	AAR58226	[Ala27]-hPTH(1-36)
261	26	86.7	38	15	AAR58154	[Val27]-hPTH(1-38)
262	26	86.7	38	15	AAR58155	[Ile27]-hPTH(1-38)
263	26	86.7	38	15	AAR58156	[Leu27]-hPTH(1-38)
264	26	86.7	38	15	AAR58157	[Arg27]-hPTH(1-38)
265	26	86.7	38	15	AAR58158	[Ala27]-hPTH(1-38)
266	25	83.3	34	14	AAR41556	[Gln26,27]hPTH (1-
267	25	83.3	34	14	AAR41566	[Arg 26,27]hPTH (1
268	25	83.3	34	14	AAR41567	[Gln26]hPTH (1-34)
269	25	83.3	34	19	AAW67290	Parathyroid hormon
270	25	83.3	36	15	AAR58290	[Ala26]-hPTH(1-36)
271	25	83.3	36	15	AAR58218	[Gln26]-hPTH(1-36)
272	25	83.3	36	15	AAR58219	[Nle26]-hPTH(1-36)
273	25	83.3	38	15	AAR58153	[Arg26]-hPTH(1-38)
274	24	80.0	28	13	AAR22064	Modified hPTH(7-34
275	24	80.0	28	13	AAR22065	Modified [Tyr_34]h
276	24	80.0	28	23	AAE23734	Human parathyroid
277	24	80.0	28	23	AAU73044	Parathyroid hormon
278	24	80.0	32	21	AAB07468	Antigenic peptide

279	24	80.0	34	14	AAR34456	Human parathyroid
280	24	80.0	34	14	AAR34457	Human parathyroid
281	24	80.0	34	14	AAR41557	[Gln25,26,27]hPTH
282	24	80.0	34	18	AAW01609	Parathyroid hormone
283	24	80.0	36	15	AAR58287	[Phe25]-hPTH(1-36)
284	24	80.0	36	15	AAR58288	[Lys25]-hPTH(1-36)
285	24	80.0	36	15	AAR58289	[Ala25]-hPTH(1-36)
286	24	80.0	36	15	AAR58192	[Gln25]-hPTH(1-36)
287	24	80.0	38	17	AAR98958	Target peptide (PT
288	23	76.7	31	17	AAR88830	Human parathyroid
289	23	76.7	32	17	AAR88840	Human parathyroid
290	23	76.7	33	17	AAR88841	Human parathyroid
291	23	76.7	34	18	AAW17949	Human parathyroid
292	23	76.7	34	18	AAW17943	Human parathyroid
293	23	76.7	34	18	AAW17945	Human parathyroid
294	23	76.7	34	18	AAW17950	Human PTH analogue
295	23	76.7	34	19	AAW67278	Parathyroid hormone
296	23	76.7	34	19	AAW67280	Parathyroid hormone
297	23	76.7	34	19	AAW67284	Parathyroid hormone
298	23	76.7	34	19	AAW67285	Parathyroid hormone
299	23	76.7	34	19	AAW67288	Parathyroid hormone
300	23	76.7	34	19	AAW67289	Parathyroid hormone
301	23	76.7	34	19	AAW67294	Parathyroid hormone
302	23	76.7	34	19	AAW67295	Parathyroid hormone
303	23	76.7	34	19	AAW67296	Parathyroid hormone
304	23	76.7	34	19	AAW67303	Parathyroid hormone
305	22	73.3	28	21	ABJ10776	Human parathyroid
306	22	73.3	30	23	AAU73136	Parathyroid hormone
307	22	73.3	30	23	AAU73137	Parathyroid hormone
308	22	73.3	33	9	AAP82176	Sequence of parath
309	22	73.3	34	13	AAR22293	Human parathyroid
310	22	73.3	34	14	AAR34358	Human parathyroid
311	22	73.3	34	14	AAR34353	Human parathyroid
312	22	73.3	34	14	AAR34354	Human parathyroid
313	22	73.3	34	14	AAR34355	Human parathyroid
314	22	73.3	34	14	AAR34356	Human parathyroid
315	22	73.3	34	14	AAR34357	Human parathyroid
316	22	73.3	34	14	AAR34359	Human parathyroid
317	22	73.3	34	14	AAR34360	Human parathyroid
318	22	73.3	34	14	AAR34361	Human parathyroid
319	22	73.3	34	14	AAR34362	Human parathyroid
320	22	73.3	34	14	AAR34363	Human parathyroid
321	22	73.3	34	14	AAR34364	Human parathyroid
322	22	73.3	34	14	AAR34365	Human parathyroid
323	22	73.3	34	14	AAR34366	Human parathyroid
324	22	73.3	34	14	AAR34367	Human parathyroid
325	22	73.3	34	14	AAR34368	Human parathyroid
326	22	73.3	34	15	AAR49697	Sequence of varian
327	22	73.3	34	15	AAR49698	Sequence of varian
328	22	73.3	34	15	AAR58187	[Phe23,His25,His26
329	22	73.3	34	15	AAR58189	[F23,H25,H26,L27,I
330	22	73.3	34	18	AAW17944	Human parathyroid
331	22	73.3	34	19	AAW67279	Parathyroid hormone
332	22	73.3	34	19	AAW67299	Parathyroid hormone
333	22	73.3	34	21	ABJ10706	Human parathyroid
334	22	73.3	34	21	ABJ10714	Human parathyroid
335	22	73.3	34	21	ABJ10717	Human parathyroid

336	22	73.3	34	21	ABJ10719	Human parathyroid
337	22	73.3	34	21	ABJ10722	Human parathyroid
338	22	73.3	34	21	ABJ10724	Human parathyroid
339	22	73.3	34	21	ABJ10727	Human parathyroid
340	22	73.3	34	21	ABJ10729	Human parathyroid
341	22	73.3	34	21	ABJ10730	Human parathyroid
342	22	73.3	34	21	ABJ10733	Human parathyroid
343	22	73.3	34	21	ABJ10736	Human parathyroid
344	22	73.3	34	21	ABJ10772	Human parathyroid
345	22	73.3	34	21	ABJ10773	Human parathyroid
346	22	73.3	34	22	AAB91085	Parathyroid hormon
347	22	73.3	34	23	AAU73100	Parathyroid hormon
348	22	73.3	34	23	AAU73101	Parathyroid hormon
349	22	73.3	36	15	AAR58266	[Nle8]-hPTH(1-36) -
350	22	73.3	36	15	AAR58267	[Phe8]-hPTH(1-36) -
351	22	73.3	36	15	AAR58268	[Cha8]-hPTH(1-36) -
352	22	73.3	36	15	AAR58285	[Ala23]-hPTH(1-36)
353	22	73.3	36	15	AAR58182	[Nva8]-hPTH(1-36) -
354	22	73.3	36	15	AAR58188	[Phe23]-hPTH(1-36)
355	22	73.3	38	15	AAR58269	[Leu8]-hPTH(1-38) -
356	21	70.0	30	23	AAU73138	Parathyroid hormon
357	21	70.0	30	23	AAU73139	Parathyroid hormon
358	21	70.0	31	19	AAW42063	Human parathyroid
359	21	70.0	31	19	AAW42065	Human parathyroid
360	21	70.0	31	19	AAW42066	Human parathyroid
361	21	70.0	34	19	AAW67305	Parathyroid hormon
362	21	70.0	34	19	AAW67302	Parathyroid hormon
363	21	70.0	34	19	AAW67304	Parathyroid hormon
364	21	70.0	34	23	AAU73102	Parathyroid hormon
365	21	70.0	34	23	AAU73103	Parathyroid hormon
366	21	70.0	34	23	AAU73104	Parathyroid hormon
367	21	70.0	34	23	AAU73140	Parathyroid hormon
368	21	70.0	36	15	AAR58217	[Ala22]-hPTH(1-36)
369	21	70.0	38	15	AAR58145	[Gly22]-hPTH(1-38)
370	21	70.0	38	15	AAR58146	[Leu22]-hPTH(1-38)
371	21	70.0	38	15	AAR58147	[His22]-hPTH(1-38)
372	21	70.0	38	15	AAR58148	[Ala22]-hPTH(1-38)
373	21	70.0	38	15	AAR58149	[Ile22]-hPTH(1-38)
374	21	70.0	38	15	AAR58150	[Val22]-hPTH(1-38)
375	21	70.0	38	15	AAR58151	[Ser22]-hPTH(1-38)
376	21	70.0	38	15	AAR58152	[Arg22]-hPTH(1-38)
377	20	66.7	34	17	AAW15812	[Trp(10)]-hPTH(1-3
378	20	66.7	34	18	AAW24276	Parathyroid hormon
379	20	66.7	34	18	AAW08120	Human PTH derivati
380	20	66.7	34	18	AAW08109	Human parathyroid
381	20	66.7	34	18	AAW08114	Human PTH derivati
382	20	66.7	34	18	AAW08118	Human PTH derivati
383	20	66.7	34	18	AAW08119	Human PTH derivati
384	20	66.7	36	15	AAR58201	[Ala10]-hPTH(1-36)
385	20	66.7	36	15	AAR58216	[Ala21]-hPTH(1-36)
386	20	66.7	38	15	AAR58138	[Ala21]-hPTH(1-38)
387	20	66.7	38	15	AAR58139	[Gly21]-hPTH(1-38)
388	20	66.7	38	15	AAR58140	[Phe21]-hPTH(1-38)
389	20	66.7	38	15	AAR58141	[Leu21]-hPTH(1-38)
390	20	66.7	38	15	AAR58142	[Asn21]-hPTH(1-38)
391	20	66.7	38	15	AAR58143	[Gln21]-hPTH(1-38)
392	20	66.7	38	15	AAR58144	[Ser21]-hPTH(1-38)

393	19	63.3	30	23	AAU73052	Parathyroid hormon
394	19	63.3	30	23	AAU73053	Parathyroid hormon
395	19	63.3	31	17	AAR88831	Human parathyroid
396	19	63.3	34	13	AAR22292	Human parathyroid
397	19	63.3	34	13	AAR22294	Human parathyroid
398	19	63.3	34	13	AAR22296	Human parathyroid
399	19	63.3	34	15	AAR58193	[L8,D10,K11,T33,A3
400	19	63.3	34	15	AAR58194	[A1,H5,L8,D10,K11,
401	19	63.3	34	18	AAW08108	Human parathyroid
402	19	63.3	34	18	AAW08113	Human PTH derivati
403	19	63.3	34	18	AAW08117	Human PTH derivati
404	19	63.3	34	18	AAW17941	Human parathyroid
405	19	63.3	34	18	AAW17939	Human parathyroid
406	19	63.3	34	19	AAW67274	Parathyroid hormon
407	19	63.3	34	19	AAW67276	Parathyroid hormon
408	19	63.3	34	21	ABJ10713	Human parathyroid
409	19	63.3	34	21	ABJ10737	Human parathyroid
410	19	63.3	34	21	ABJ10769	Human parathyroid
411	19	63.3	34	23	AAU73029	Parathyroid hormon
412	19	63.3	34	23	AAU73030	Parathyroid hormon
413	19	63.3	35	23	AAU73173	Parathyroid hormon
414	19	63.3	35	23	AAU73174	Parathyroid hormon
415	19	63.3	36	15	AAR58271	[Ala11]-hPTH(1-36)
416	19	63.3	36	15	AAR58279	[Lys20]-hPTH(1-36)
417	19	63.3	38	15	AAR58137	[Phe20]-hPTH(1-38)
418	18	60.0	28	13	AAR22066	Modified [D-Trp_12
419	18	60.0	28	21	AAV98046	Human parathyroid
420	18	60.0	30	23	AAU73054	Parathyroid hormon
421	18	60.0	34	11	AAR08300	Human parathyroid
422	18	60.0	34	11	AAR08303	Human parathyroid
423	18	60.0	34	13	AAR22297	Human parathyroid
424	18	60.0	34	18	AAW08121	Human PTH derivati
425	18	60.0	34	18	AAW08115	Human PTH derivati
426	18	60.0	34	18	AAW08116	Human PTH derivati
427	18	60.0	34	18	AAW17954	Human parathyroid
428	18	60.0	34	18	AAW17959	Human parathyroid
429	18	60.0	34	22	AAB84771	Parathyroid hormon
430	18	60.0	34	22	AAB84826	Parathyroid hormon
431	18	60.0	34	22	AAB96893	Rat parathyroid ho
432	18	60.0	34	22	AAB96916	Parathyroid hormon
433	18	60.0	34	22	AAB96919	Parathyroid hormon
434	18	60.0	34	22	AAB96930	Rat parathyroid ho
435	18	60.0	34	23	AAU73031	Parathyroid hormon
436	18	60.0	35	23	AAU73175	Parathyroid hormon
437	18	60.0	36	15	AAR58203	[Ala12]-hPTH(1-36)
438	18	60.0	36	15	AAR58214	[Ala19]-hPTH(1-36)
439	18	60.0	38	15	AAR58136	[Arg19]-hPTH(1-38)
440	18	60.0	38	15	AAR58089	[Arg12]-hPTH(1-38)
441	18	60.0	38	15	AAR58090	[Ser12]-hPTH(1-38)
442	18	60.0	38	15	AAR58123	[Ser19]-hPTH(1-38)
443	18	60.0	38	15	AAR58124	[Lys19]-hPTH(1-38)
444	18	60.0	38	15	AAR58125	[Leu19]-hPTH(1-38)
445	18	60.0	38	15	AAR58126	[Ala19]-hPTH(1-38)
446	18	60.0	38	15	AAR58127	[Tyr19]-hPTH(1-38)
447	18	60.0	38	15	AAR58128	[Met19]-hPTH(1-38)
448	18	60.0	38	15	AAR58129	[His19]-hPTH(1-38)
449	18	60.0	38	15	AAR58130	[Val19]-hPTH(1-38)

450	18	60.0	38	15	AAR58131	[Gly19]-hPTH(1-38)
451	18	60.0	38	15	AAR58132	[Pro19]-hPTH(1-38)
452	18	60.0	38	15	AAR58133	[Asp19]-hPTH(1-38)
453	18	60.0	38	15	AAR58134	[Ile19]-hPTH(1-38)
454	18	60.0	38	15	AAR58135	[Val19,Gln24]-hPTH
455	17	56.7	28	21	AAV98041	Human parathyroid
456	17	56.7	28	21	AAV98042	Human parathyroid
457	17	56.7	28	21	AAV98044	Human parathyroid
458	17	56.7	30	6	AAP50665	Human parathyroid
459	17	56.7	34	13	AAR22291	Human parathyroid
460	17	56.7	34	18	AAW08112	Human PTH derivati
461	17	56.7	34	19	AAW67298	Parathyroid hormon
462	17	56.7	34	19	AAW67300	Parathyroid hormon
463	17	56.7	34	19	AAW67301	Parathyroid hormon
464	17	56.7	34	21	ABJ10742	Human parathyroid
465	17	56.7	34	22	AAB91087	Parathyroid hormon
466	17	56.7	36	15	AAR58277	[Nle18]-hPTH(1-36)
467	17	56.7	36	15	AAR58204	[Gln13]-hPTH(1-36)
468	17	56.7	36	15	AAR58205	[His13]-hPTH(1-36)
469	17	56.7	36	15	AAR58206	[Leu13]-hPTH(1-36)
470	17	56.7	36	15	AAR58207	[Ala13]-hPTH(1-36)
471	17	56.7	36	15	AAR58183	[Gln18]-hPTH(1-36)
472	17	56.7	36	15	AAR58184	[Tyr18]-hPTH(1-36)
473	17	56.7	36	15	AAR58185	[Lys18]-hPTH(1-36)
474	17	56.7	36	15	AAR58186	[Ala18]-hPTH(1-36)
475	17	56.7	38	15	AAR58091	[Cys13]-hPTH(1-38)
476	17	56.7	38	15	AAR58092	[Ile13]-hPTH(1-38)
477	17	56.7	38	15	AAR58093	[Asn13]-hPTH(1-38)
478	17	56.7	38	15	AAR58094	[Trp13]-hPTH(1-38)
479	17	56.7	38	15	AAR58095	[Asp13]-hPTH(1-38)
480	17	56.7	38	15	AAR58096	[Val13]-hPTH(1-38)
481	17	56.7	38	15	AAR58097	[Thr13]-hPTH(1-38)
482	17	56.7	38	15	AAR58098	[Ser13]-hPTH(1-38)
483	17	56.7	38	15	AAR58099	[Tyr13]-hPTH(1-38)
484	17	56.7	38	15	AAR58100	[Met13]-hPTH(1-38)
485	17	56.7	38	15	AAR58101	[Gln13]-hPTH(1-38)
486	17	56.7	38	15	AAR58102	[Leu13]-hPTH(1-38)
487	17	56.7	38	15	AAR58103	[Ala13]-hPTH(1-38)
488	17	56.7	38	15	AAR58104	[Gly13]-hPTH(1-38)
489	16	53.3	28	22	AAB81078	Human parathyroid
490	16	53.3	28	23	AAU73105	Parathyroid hormon
491	16	53.3	28	23	AAU73106	Parathyroid hormon
492	16	53.3	31	21	AAV96973	Parathyroid hormon
493	16	53.3	31	21	AAV96974	Parathyroid hormon
494	16	53.3	31	22	AAB81077	Human parathyroid
495	16	53.3	34	17	AAW14310	Cyclic parathyroid
496	16	53.3	34	17	AAW14311	Cyclic parathyroid
497	16	53.3	34	18	AAW08129	Human PTH derivati
498	16	53.3	34	18	AAW17958	Human parathyroid
499	16	53.3	34	19	AAW48394	Human PTH/PTHrP hy
500	16	53.3	34	22	AAB84775	Parathyroid hormon
501	16	53.3	34	22	AAB96922	Parathyroid hormon
502	16	53.3	36	15	AAR58209	[Ala14]-hPTH(1-36)
503	16	53.3	36	15	AAR58212	[Ala17]-hPTH(1-36)
504	16	53.3	38	15	AAR58037	[Ser14]-hPTH(1-38)
505	16	53.3	38	15	AAR58105	[Val14]-hPTH(1-38)
506	16	53.3	38	15	AAR58106	[Ala14]-hPTH(1-38)

507	16	53.3	38	15	AAR58107	[Lys14]-hPTH(1-38)
508	16	53.3	38	15	AAR58108	[Arg14]-hPTH(1-38)
509	16	53.3	38	15	AAR58109	[Thr14]-hPTH(1-38)
510	16	53.3	38	15	AAR58110	[Ile14]-hPTH(1-38)
511	16	53.3	38	15	AAR58111	[Tyr14]-hPTH(1-38)
512	16	53.3	38	15	AAR58120	[Ala17]-hPTH(1-38)
513	16	53.3	38	15	AAR58121	[Met17]-hPTH(1-38)
514	16	53.3	38	15	AAR58122	[Ile17]-hPTH(1-38)
515	15	50.0	28	23	AAU73107	Parathyroid hormone
516	15	50.0	28	23	AAU73108	Parathyroid hormone
517	15	50.0	28	23	AAU73109	Parathyroid hormone
518	15	50.0	30	23	AAU73059	Parathyroid hormone
519	15	50.0	34	14	AAR41551	[Thr16]hPTH (1-34)
520	15	50.0	34	14	AAR41552	[Glu16]hPTH (1-34)
521	15	50.0	34	14	AAR41553	[Lys16]hPTH (1-34)
522	15	50.0	34	14	AAR41561	[Lys16, Gln27]hPTH
523	15	50.0	34	14	AAR41562	[Orn16, Gln27]hPTH
524	15	50.0	34	14	AAR41563	[Hci16, Gln27]hPTH
525	15	50.0	34	14	AAR41564	[Asp16, Gln27]hPTH
526	15	50.0	34	14	AAR41565	[Arg16, Gln27]hPTH
527	15	50.0	34	14	AAR41571	[D-Lys16]hPTH (1-3
528	15	50.0	34	14	AAR41573	[Gln16]hPTH (1-34)
529	15	50.0	34	14	AAR41574	[Ser16]hPTH (1-34)
530	15	50.0	34	14	AAR41575	[Gly16]hPTH (1-34)
531	15	50.0	34	14	AAR41576	[Lys16]hPTH (1-34)
532	15	50.0	34	14	AAR41577	[Lys16, Asp17]hPTH
533	15	50.0	34	14	AAR41580	[Lys16,17]hPTH (1-
534	15	50.0	34	14	AAR41581	[Arg16,17]hPTH (1-
535	15	50.0	34	17	AAR99981	Porcine parathyroi
536	15	50.0	34	18	AAW08132	Human PTH derivati
537	15	50.0	34	18	AAW17942	Human parathyroid
538	15	50.0	34	18	AAW17967	Human PTH analogue
539	15	50.0	34	18	AAW17952	Human parathyroid
540	15	50.0	34	18	AAW17953	Human parathyroid
541	15	50.0	34	18	AAW17956	Human parathyroid
542	15	50.0	34	19	AAW67277	Parathyroid hormone
543	15	50.0	34	19	AAW67287	Parathyroid hormone
544	15	50.0	34	19	AAW61660	Parathyroid hormone
545	15	50.0	34	19	AAW65977	Porcine parathyroi
546	15	50.0	34	19	AAW42616	Porcine parathyroi
547	15	50.0	34	20	AAW81873	Porcine PTH N-term
548	15	50.0	34	23	AAU73036	Parathyroid hormone
549	15	50.0	36	15	AAR58274	[Ala15]-hPTH(1-36)
550	15	50.0	36	15	AAR58275	[Ala16]-hPTH(1-36)
551	15	50.0	37	22	AAB86232	Porcine parathyroi
552	15	50.0	38	15	AAR58061	[Ile15]-hPTH(1-38)
553	15	50.0	38	15	AAR58036	[Gln16]-hPTH(1-38)
554	15	50.0	38	15	AAR58112	[Tyr15]-hPTH(1-38)
555	15	50.0	38	15	AAR58113	[Arg15]-hPTH(1-38)
556	15	50.0	38	15	AAR58114	[Val15]-hPTH(1-38)
557	15	50.0	38	15	AAR58115	[Lys16]-hPTH(1-38)
558	15	50.0	38	15	AAR58116	[Ser16]-hPTH(1-38)
559	15	50.0	38	15	AAR58117	[Leu16]-hPTH(1-38)
560	15	50.0	38	15	AAR58118	[Ala16]-hPTH(1-38)
561	15	50.0	38	15	AAR58119	[Gly16]-hPTH(1-38)
562	14	46.7	28	13	AAR22058	Modified bovine PT
563	14	46.7	28	13	AAR22059	Modified [Tyr_34]b

564	14	46.7	28	13	AAR22060	Modified [D-Trp_12
565	14	46.7	28	22	AAB91115	Parathyroid hormon
566	14	46.7	28	23	AAE18405	Bovine PTH peptide
567	14	46.7	28	23	AAU73046	Parathyroid hormon
568	14	46.7	28	23	AAU73047	Parathyroid hormon
569	14	46.7	28	23	AAU73050	Parathyroid hormon
570	14	46.7	28	23	AAU73066	Parathyroid hormon
571	14	46.7	30	23	AAU73057	Parathyroid hormon
572	14	46.7	30	23	AAU73060	Parathyroid hormon
573	14	46.7	31	5	AAP40510	Bovine parathyroid
574	14	46.7	31	21	AAV96975	Parathyroid hormon
575	14	46.7	32	22	AAB91096	Parathyroid hormon
576	14	46.7	32	23	AAE23739	Bovine parathyroid
577	14	46.7	32	23	AAE18402	Bovine PTH peptide
578	14	46.7	32	23	AAU73042	Parathyroid hormon
579	14	46.7	34	9	AAP82177	Sequence of parath
580	14	46.7	34	11	AAR07917	Rat parathyroid ho
581	14	46.7	34	11	AAR07918	Bovine parathyroid
582	14	46.7	34	11	AAR07920	Rat parathyroid ho
583	14	46.7	34	11	AAR07921	Bovine parathyroid
584	14	46.7	34	11	AAR08299	Bovine parathyroid
585	14	46.7	34	11	AAR08302	Bovine parathyroid
586	14	46.7	34	14	AAR41568	[Lys15,16 His27]hP
587	14	46.7	34	14	AAR41569	[Lys15, His27]hPTH
588	14	46.7	34	14	AAR41572	[Lys15,16,17, His2
589	14	46.7	34	14	AAR41579	[Lys15,15,17]hPTH
590	14	46.7	34	14	AAR41582	[Arg15,16,17]hPTH
591	14	46.7	34	16	AAR62432	Accelerator peptid
592	14	46.7	34	17	AAR99979	Bovine parathyroid
593	14	46.7	34	17	AAR99980	Rat parathyroid ho
594	14	46.7	34	18	AAW08124	Human PTH derivati
595	14	46.7	34	18	AAW08111	Human PTH derivati
596	14	46.7	34	18	AAW19996	Cyclised rat parat
597	14	46.7	34	18	AAW19995	Cyclised bovine pa
598	14	46.7	34	18	AAW20001	Cyclised bovine pa
599	14	46.7	34	18	AAW20002	Cyclised rat parat
600	14	46.7	34	18	AAW20007	Cyclised bovine pa
601	14	46.7	34	18	AAW20008	Cyclised rat parat
602	14	46.7	34	18	AAW17963	Human PTH analogue
603	14	46.7	34	19	AAW61659	Parathyroid hormon
604	14	46.7	34	19	AAW65976	Bovine parathyroid
605	14	46.7	34	19	AAW42615	Bovine parathyroid
606	14	46.7	34	19	AAW48398	Human PTH/PTHrP hy
607	14	46.7	34	20	AAW81872	Bovine PTH N-termi
608	14	46.7	34	22	AAB84777	Native human parat
609	14	46.7	34	22	AAB96897	Rat parathyroid ho
610	14	46.7	34	22	AAB91100	Parathyroid hormon
611	14	46.7	34	23	AAE23738	Bovine parathyroid
612	14	46.7	34	23	AAE18394	Bovine PTH peptide
613	14	46.7	34	23	AAU73034	Parathyroid hormon
614	14	46.7	34	23	AAU73037	Parathyroid hormon
615	14	46.7	34	24	ABP71489	Parathyroid hormon
616	14	46.7	34	24	ABP71499	Rat parathyroid ho
617	14	46.7	36	15	AAR58071	[Aib3, Gln18]-hPTH
618	14	46.7	36	15	AAR58088	[1-amino-cyclopent
619	14	46.7	37	22	AAB86230	Bovine parathyroid
620	14	46.7	37	22	AAB86231	Rat parathyroid ho

621	14	46.7	37	22	AAB86233	Canine parathyroid
622	14	46.7	37	23	ABB82204	Bovine parathyroid
623	13	43.3	34	14	AAR41578	[Lys14,15,16,17]hP
624	13	43.3	34	15	AAR58195	[S14,I15,Q16,D17,L
625	13	43.3	34	17	AAW14308	Cyclic parathyroid
626	13	43.3	34	17	AAW14309	Cyclic parathyroid
627	13	43.3	34	17	AAW14312	Cyclic parathyroid
628	13	43.3	34	17	AAW14313	Cyclic parathyroid
629	13	43.3	34	17	AAW14314	Cyclic parathyroid
630	13	43.3	34	17	AAW14315	Cyclic parathyroid
631	13	43.3	34	18	AAW08122	Human PTH derivati
632	13	43.3	34	18	AAW08123	Human PTH derivati
633	12	40.0	28	13	AAR22061	Modified [Nle_8,18
634	12	40.0	28	13	AAR22062	Modified [Nle_8,18
635	12	40.0	28	13	AAR22067	Modified [Nle_8,_1
636	12	40.0	28	13	AAR22068	Modified [Nle_8,_1
637	12	40.0	28	21	ABJ10774	Human parathyroid
638	12	40.0	28	21	ABJ10775	Human parathyroid
639	12	40.0	28	23	AAE18404	Bovine PTH peptide
640	12	40.0	28	23	AAU73045	Parathyroid hormon
641	12	40.0	28	23	AAU73048	Parathyroid hormon
642	12	40.0	28	23	AAU73049	Parathyroid hormon
643	12	40.0	28	23	AAU73065	Parathyroid hormon
644	12	40.0	28	23	AAU73067	Parathyroid hormon
645	12	40.0	30	22	AAB91089	Parathyroid hormon
646	12	40.0	30	22	AAB91092	Parathyroid hormon
647	12	40.0	30	23	AAU73056	Parathyroid hormon
648	12	40.0	30	23	AAU73058	Parathyroid hormon
649	12	40.0	31	5	AAP40511	Bovine parathyroid
650	12	40.0	31	5	AAP40761	Human parathyroid
651	12	40.0	32	22	AAB91088	Parathyroid hormon
652	12	40.0	32	22	AAB91090	Parathyroid hormon
653	12	40.0	32	22	AAB91091	Parathyroid hormon
654	12	40.0	32	23	AAE18403	Bovine PTH peptide
655	12	40.0	32	23	AAU73041	Parathyroid hormon
656	12	40.0	32	23	AAU73043	Parathyroid hormon
657	12	40.0	33	17	AAW15814	[Leu(8),Trp(10),Al
658	12	40.0	34	6	AAP50517	Sequence of methio
659	12	40.0	34	11	AAR07924	Bovine parathyroid
660	12	40.0	34	11	AAR07925	Human parathyroid
661	12	40.0	34	11	AAR08305	Bovine parathyroid
662	12	40.0	34	11	AAR08306	Human parathyroid
663	12	40.0	34	13	AAR22295	Human parathyroid
664	12	40.0	34	14	AAV18002	Human PTH(1-34) de
665	12	40.0	34	15	AAR45528	Parathyroid hormon
666	12	40.0	34	15	AAR58239	Isopropyl- [Nle8,18
667	12	40.0	34	15	AAR58241	[Nle8,18,D-Asn33,D
668	12	40.0	34	15	AAR55817	[L8,Q18,T33,A34]-h
669	12	40.0	34	15	AAR55819	[L8,A16,Q18,T33,A3
670	12	40.0	34	15	AAR55821	[L8,D10,K11,Q18,T3
671	12	40.0	34	15	AAR55823	[L8,D10,K11,A16,Q1
672	12	40.0	34	15	AAR58021	[L8,D10,A16,Q18,T3
673	12	40.0	34	15	AAR58034	Isopropyl- [L8,K(Is
674	12	40.0	34	16	AAR69055	PTH analogue with
675	12	40.0	34	17	AAW15813	[Leu(8),Trp(10),Al
676	12	40.0	34	17	AAW15815	[Leu(8),Trp(10),DL
677	12	40.0	34	17	AAW15828	N-alpha-acylated [

678	12	40.0	34	17	AAW14316	Cyclic parathyroid
679	12	40.0	34	18	AAW13352	Truncated parathyr
680	12	40.0	34	18	AAW12651	Parathyroid hormon
681	12	40.0	34	18	AAW20004	Cyclised [Nle 8,18
682	12	40.0	34	18	AAW19997	Cyclised [Nle 8,18
683	12	40.0	34	18	AAW19998	Cyclised [Nle 8,18
684	12	40.0	34	18	AAW20003	Cyclised [Nle 8,18
685	12	40.0	34	18	AAW20009	Cyclised [Nle 8,18
686	12	40.0	34	18	AAW20010	Cyclised [Nle 8,18
687	12	40.0	34	18	AAW17940	Human PTH analogue
688	12	40.0	34	18	AAW17970	Human PTH analogue
689	12	40.0	34	18	AAW17964	Human PTH analogue
690	12	40.0	34	19	AAW67275	Parathyroid hormon
691	12	40.0	34	19	AAW61725	Parathyroid hormon
692	12	40.0	34	19	AAW66053	Parathyroid hormon
693	12	40.0	34	19	AAW42602	Parathyroid hormon
694	12	40.0	34	19	AAW48395	Human PTH/PTHrP hy
695	12	40.0	34	20	AAW02587	Parathyroid hormon
696	12	40.0	34	20	AAW92218	Analogue of parath
697	12	40.0	34	20	AAW92219	Analogue of parath
698	12	40.0	34	20	AAW03920	Analogue of parath
699	12	40.0	34	20	AAW03921	Analogue of parath
700	12	40.0	34	20	AAW03922	Analogue of parath
701	12	40.0	34	20	AAW03923	Analogue of parath
702	12	40.0	34	20	AAW03924	Analogue of parath
703	12	40.0	34	20	AAW03925	Analogue of parath
704	12	40.0	34	20	AAW03926	Analogue of parath
705	12	40.0	34	20	AAW03927	Analogue of parath
706	12	40.0	34	20	AAW03928	Analogue of parath
707	12	40.0	34	20	AAW03929	Analogue of parath
708	12	40.0	34	20	AAW03930	Analogue of parath
709	12	40.0	34	20	AAW03931	Analogue of parath
710	12	40.0	34	20	AAW03932	Analogue of parath
711	12	40.0	34	20	AAW03933	Analogue of parath
712	12	40.0	34	20	AAW92236	Analogue of parath
713	12	40.0	34	20	AAW92237	Analogue of parath
714	12	40.0	34	20	AAW92238	Analogue of parath
715	12	40.0	34	20	AAW92239	Analogue of parath
716	12	40.0	34	20	AAW92240	Analogue of parath
717	12	40.0	34	20	AAW92241	Analogue of parath
718	12	40.0	34	20	AAW92242	Analogue of parath
719	12	40.0	34	20	AAW92243	Analogue of parath
720	12	40.0	34	20	AAW92244	Analogue of parath
721	12	40.0	34	20	AAW92245	Analogue of parath
722	12	40.0	34	20	AAW92246	Analogue of parath
723	12	40.0	34	20	AAW92247	Analogue of parath
724	12	40.0	34	20	AAW92248	Analogue of parath
725	12	40.0	34	20	AAW92249	Analogue of parath
726	12	40.0	34	20	AAW92250	Analogue of parath
727	12	40.0	34	20	AAW03919	Analogue of parath
728	12	40.0	34	20	AAW92220	Analogue of parath
729	12	40.0	34	20	AAW92221	Analogue of parath
730	12	40.0	34	20	AAW92222	Analogue of parath
731	12	40.0	34	20	AAW92223	Analogue of parath
732	12	40.0	34	20	AAW92224	Analogue of parath
733	12	40.0	34	20	AAW92225	Analogue of parath
734	12	40.0	34	20	AAW92226	Analogue of parath

735	12	40.0	34	20	AAW92227	Analogue of parath
736	12	40.0	34	20	AAW92228	Analogue of parath
737	12	40.0	34	20	AAW92229	Analogue of parath
738	12	40.0	34	20	AAW92230	Analogue of parath
739	12	40.0	34	20	AAW92231	Analogue of parath
740	12	40.0	34	20	AAW92232	Analogue of parath
741	12	40.0	34	20	AAW92233	Analogue of parath
742	12	40.0	34	20	AAW92234	Analogue of parath
743	12	40.0	34	20	AAW92235	Analogue of parath
744	12	40.0	34	20	AAW92236	Analogue of parath
745	12	40.0	34	20	AAW92237	Analogue of parath
746	12	40.0	34	20	AAW92238	Analogue of parath
747	12	40.0	34	20	AAW92239	Analogue of parath
748	12	40.0	34	20	AAW92240	Analogue of parath
749	12	40.0	34	20	AAW92241	Analogue of parath
750	12	40.0	34	20	AAW92242	Analogue of parath
751	12	40.0	34	20	AAW92243	Analogue of parath
752	12	40.0	34	20	AAW92244	Analogue of parath
753	12	40.0	34	20	AAW92245	Analogue of parath
754	12	40.0	34	20	AAW92246	Analogue of parath
755	12	40.0	34	20	AAW92247	Analogue of parath
756	12	40.0	34	20	AAW92248	Analogue of parath
757	12	40.0	34	20	AAW92249	Analogue of parath
758	12	40.0	34	20	AAW92250	Analogue of parath
759	12	40.0	34	20	AAW92251	Analogue of parath
760	12	40.0	34	20	AAW92252	Analogue of parath
761	12	40.0	34	20	AAW92253	Analogue of parath
762	12	40.0	34	20	AAW92254	Analogue of parath
763	12	40.0	34	20	AAW92255	Analogue of parath
764	12	40.0	34	20	AAW92256	Analogue of parath
765	12	40.0	34	20	AAW92257	Analogue of parath
766	12	40.0	34	20	AAW92258	Analogue of parath
767	12	40.0	34	20	AAW92259	Analogue of parath
768	12	40.0	34	20	AAW92260	Analogue of parath
769	12	40.0	34	20	AAW92261	Analogue of parath
770	12	40.0	34	20	AAW92262	Analogue of parath
771	12	40.0	34	20	AAW92263	Analogue of parath
772	12	40.0	34	20	AAW92264	Analogue of parath
773	12	40.0	34	20	AAW92265	Analogue of parath
774	12	40.0	34	20	AAW92266	Analogue of parath
775	12	40.0	34	20	AAW92267	Analogue of parath
776	12	40.0	34	20	AAW92268	Analogue of parath
777	12	40.0	34	20	AAW92269	Analogue of parath
778	12	40.0	34	20	AAW92270	Analogue of parath
779	12	40.0	34	20	AAW92271	Analogue of parath
780	12	40.0	34	20	AAW92272	Analogue of parath
781	12	40.0	34	20	AAW92273	Analogue of parath
782	12	40.0	34	20	AAW92274	Analogue of parath
783	12	40.0	34	20	AAW92275	Analogue of parath
784	12	40.0	34	20	AAW92276	Analogue of parath
785	12	40.0	34	20	AAW92277	Analogue of parath
786	12	40.0	34	20	AAW92278	Analogue of parath
787	12	40.0	34	20	AAW92279	Analogue of parath
788	12	40.0	34	20	AAW92280	Analogue of parath
789	12	40.0	34	20	AAW92281	Analogue of parath
790	12	40.0	34	20	AAW92282	Analogue of parath
791	12	40.0	34	20	AAW92283	Analogue of parath

792	12	40.0	34	20	AAW92167	Analogue of parath
793	12	40.0	34	20	AAW92188	Analogue of parath
794	12	40.0	34	20	AAW92189	Analogue of parath
795	12	40.0	34	20	AAW92190	Analogue of parath
796	12	40.0	34	20	AAW92191	Analogue of parath
797	12	40.0	34	20	AAW92192	Analogue of parath
798	12	40.0	34	20	AAW92193	Analogue of parath
799	12	40.0	34	20	AAW92194	Analogue of parath
800	12	40.0	34	20	AAW92195	Analogue of parath
801	12	40.0	34	20	AAW92196	Analogue of parath
802	12	40.0	34	20	AAW92197	Analogue of parath
803	12	40.0	34	20	AAW92166	Analogue of parath
804	12	40.0	34	20	AAW92168	Analogue of parath
805	12	40.0	34	20	AAW92169	Analogue of parath
806	12	40.0	34	20	AAW92170	Analogue of parath
807	12	40.0	34	20	AAW92171	Analogue of parath
808	12	40.0	34	20	AAW92172	Analogue of parath
809	12	40.0	34	20	AAW92173	Analogue of parath
810	12	40.0	34	20	AAW92174	Analogue of parath
811	12	40.0	34	20	AAW92175	Analogue of parath
812	12	40.0	34	20	AAW92176	Analogue of parath
813	12	40.0	34	20	AAW92177	Analogue of parath
814	12	40.0	34	20	AAW92178	Analogue of parath
815	12	40.0	34	20	AAW92179	Analogue of parath
816	12	40.0	34	20	AAW92180	Analogue of parath
817	12	40.0	34	20	AAW92181	Analogue of parath
818	12	40.0	34	20	AAW92182	Analogue of parath
819	12	40.0	34	20	AAW92152	Analogue of parath
820	12	40.0	34	20	AAW92150	Analogue of parath
821	12	40.0	34	20	AAW92151	Analogue of parath
822	12	40.0	34	20	AAW92153	Analogue of parath
823	12	40.0	34	20	AAW92154	Analogue of parath
824	12	40.0	34	20	AAW92155	Analogue of parath
825	12	40.0	34	20	AAW92156	Analogue of parath
826	12	40.0	34	20	AAW92157	Analogue of parath
827	12	40.0	34	20	AAW92158	Analogue of parath
828	12	40.0	34	20	AAW92159	Analogue of parath
829	12	40.0	34	20	AAW92160	Analogue of parath
830	12	40.0	34	20	AAW92161	Analogue of parath
831	12	40.0	34	20	AAW92162	Analogue of parath
832	12	40.0	34	20	AAW92163	Analogue of parath
833	12	40.0	34	20	AAW92164	Analogue of parath
834	12	40.0	34	20	AAW92165	Analogue of parath
835	12	40.0	34	20	AAW92148	Analogue of parath
836	12	40.0	34	20	AAW92149	Analogue of parath
837	12	40.0	34	20	AAW74396	Modified parathyro
838	12	40.0	34	20	AAW81945	Synthetic PTH and
839	12	40.0	34	21	ABJ10705	Human parathyroid
840	12	40.0	34	21	ABJ10707	Human parathyroid
841	12	40.0	34	21	ABJ10708	Human parathyroid
842	12	40.0	34	21	ABJ10709	Human parathyroid
843	12	40.0	34	21	ABJ10710	Human parathyroid
844	12	40.0	34	21	ABJ10711	Human parathyroid
845	12	40.0	34	21	ABJ10715	Human parathyroid
846	12	40.0	34	21	ABJ10716	Human parathyroid
847	12	40.0	34	21	ABJ10718	Human parathyroid
848	12	40.0	34	21	ABJ10720	Human parathyroid

849	12	40.0	34	21	ABJ10721	Human parathyroid
850	12	40.0	34	21	ABJ10723	Human parathyroid
851	12	40.0	34	21	ABJ10725	Human parathyroid
852	12	40.0	34	21	ABJ10726	Human parathyroid
853	12	40.0	34	21	ABJ10728	Human parathyroid
854	12	40.0	34	21	ABJ10731	Human parathyroid
855	12	40.0	34	21	ABJ10732	Human parathyroid
856	12	40.0	34	21	ABJ10734	Human parathyroid
857	12	40.0	34	21	ABJ10735	Human parathyroid
858	12	40.0	34	21	ABJ10738	Human parathyroid
859	12	40.0	34	21	ABJ10739	Human parathyroid
860	12	40.0	34	21	ABJ10740	Human parathyroid
861	12	40.0	34	21	ABJ10741	Human parathyroid
862	12	40.0	34	21	ABJ10743	Human parathyroid
863	12	40.0	34	21	ABJ10744	Human parathyroid
864	12	40.0	34	21	ABJ10745	Human parathyroid
865	12	40.0	34	21	ABJ10746	Human parathyroid
866	12	40.0	34	21	ABJ10747	Human parathyroid
867	12	40.0	34	21	ABJ10748	Human parathyroid
868	12	40.0	34	21	ABJ10749	Human parathyroid
869	12	40.0	34	21	ABJ10750	Human parathyroid
870	12	40.0	34	21	ABJ10751	Human parathyroid
871	12	40.0	34	21	ABJ10752	Human parathyroid
872	12	40.0	34	21	ABJ10753	Human parathyroid
873	12	40.0	34	21	ABJ10754	Human parathyroid
874	12	40.0	34	21	ABJ10755	Human parathyroid
875	12	40.0	34	21	ABJ10756	Human parathyroid
876	12	40.0	34	21	ABJ10761	Human parathyroid
877	12	40.0	34	21	ABJ10762	Human parathyroid
878	12	40.0	34	21	ABJ10763	Human parathyroid
879	12	40.0	34	21	ABJ10764	Human parathyroid
880	12	40.0	34	21	ABJ10765	Human parathyroid
881	12	40.0	34	21	ABJ10766	Human parathyroid
882	12	40.0	34	21	ABJ10767	Human parathyroid
883	12	40.0	34	21	ABJ10768	Human parathyroid
884	12	40.0	34	21	ABJ10771	Human parathyroid
885	12	40.0	34	21	ABJ10777	Human parathyroid
886	12	40.0	34	22	AAB91084	Parathyroid hormon
887	12	40.0	34	23	AAE18396	Bovine PTH peptide
888	12	40.0	34	23	AAE18397	Human PTH peptide
889	12	40.0	34	23	AAU73033	Parathyroid hormon
890	12	40.0	34	23	AAU73035	Parathyroid hormon
891	12	40.0	34	24	ABP71490	Parathyroid hormon
892	12	40.0	34	24	ABP71491	Parathyroid hormon
893	12	40.0	34	24	ABP71492	Parathyroid hormon
894	12	40.0	34	24	ABP71494	Parathyroid hormon
895	12	40.0	35	2	AAP10140	h-PTH antigen. Sy
896	12	40.0	35	16	AAR74512	Parathyroid hormon
897	12	40.0	35	16	AAR74513	Parathyroid hormon
898	12	40.0	35	16	AAR74514	Parathyroid hormon
899	12	40.0	35	16	AAR74515	Parathyroid hormon
900	12	40.0	35	16	AAR74516	Parathyroid hormon
901	12	40.0	35	16	AAR74517	Parathyroid hormon
902	12	40.0	35	16	AAR74518	Parathyroid hormon
903	12	40.0	35	16	AAR74519	Parathyroid hormon
904	12	40.0	35	16	AAR74520	Parathyroid hormon
905	12	40.0	35	16	AAR74527	Human parathyroid

906	12	40.0	35	16	AAR74507	Parathyroid hormon
907	12	40.0	35	16	AAR74508	Parathyroid hormon
908	12	40.0	35	16	AAR74509	Parathyroid hormon
909	12	40.0	35	16	AAR74510	Parathyroid hormon
910	12	40.0	35	16	AAR74511	Parathyroid hormon
911	12	40.0	35	16	AAR74464	Parathyroid hormon
912	12	40.0	35	16	AAR74465	Parathyroid hormon
913	12	40.0	35	16	AAR74466	Parathyroid hormon
914	12	40.0	35	16	AAR74467	Parathyroid hormon
915	12	40.0	35	16	AAR74468	Parathyroid hormon
916	12	40.0	35	16	AAR74469	Parathyroid hormon
917	12	40.0	35	16	AAR74470	Parathyroid hormon
918	12	40.0	35	16	AAR74471	Parathyroid hormon
919	12	40.0	35	16	AAR74472	Parathyroid hormon
920	12	40.0	35	16	AAR74473	Parathyroid hormon
921	12	40.0	35	16	AAR74474	Parathyroid hormon
922	12	40.0	35	16	AAR74475	Parathyroid hormon
923	12	40.0	35	16	AAR74476	Parathyroid hormon
924	12	40.0	35	16	AAR74477	Parathyroid hormon
925	12	40.0	35	16	AAR74478	Parathyroid hormon
926	12	40.0	35	16	AAR74479	Parathyroid hormon
927	12	40.0	35	16	AAR74448	Parathyroid hormon
928	12	40.0	35	16	AAR74449	Parathyroid hormon
929	12	40.0	35	16	AAR74450	Parathyroid hormon
930	12	40.0	35	16	AAR74451	Parathyroid hormon
931	12	40.0	35	16	AAR74452	Parathyroid hormon
932	12	40.0	35	16	AAR74453	Parathyroid hormon
933	12	40.0	35	16	AAR74454	Parathyroid hormon
934	12	40.0	35	16	AAR74455	Parathyroid hormon
935	12	40.0	35	16	AAR74456	Parathyroid hormon
936	12	40.0	35	16	AAR74457	Parathyroid hormon
937	12	40.0	35	16	AAR74458	Parathyroid hormon
938	12	40.0	35	16	AAR74459	Parathyroid hormon
939	12	40.0	35	16	AAR74460	Parathyroid hormon
940	12	40.0	35	16	AAR74461	Parathyroid hormon
941	12	40.0	35	16	AAR74462	Parathyroid hormon
942	12	40.0	35	16	AAR74463	Parathyroid hormon
943	12	40.0	35	16	AAR74432	Parathyroid hormon
944	12	40.0	35	16	AAR74433	Parathyroid hormon
945	12	40.0	35	16	AAR74434	Parathyroid hormon
946	12	40.0	35	16	AAR74435	Parathyroid hormon
947	12	40.0	35	16	AAR74436	Parathyroid hormon
948	12	40.0	35	16	AAR74437	Parathyroid hormon
949	12	40.0	35	16	AAR74438	Parathyroid hormon
950	12	40.0	35	16	AAR74439	Parathyroid hormon
951	12	40.0	35	16	AAR74440	Parathyroid hormon
952	12	40.0	35	16	AAR74441	Parathyroid hormon
953	12	40.0	35	16	AAR74442	Parathyroid hormon
954	12	40.0	35	16	AAR74443	Parathyroid hormon
955	12	40.0	35	16	AAR74444	Parathyroid hormon
956	12	40.0	35	16	AAR74445	Parathyroid hormon
957	12	40.0	35	16	AAR74446	Parathyroid hormon
958	12	40.0	35	16	AAR74447	Parathyroid hormon
959	12	40.0	35	16	AAR74429	Parathyroid hormon
960	12	40.0	35	16	AAR74430	Parathyroid hormon
961	12	40.0	35	16	AAR74431	Parathyroid hormon
962	12	40.0	35	16	AAR74398	Parathyroid hormon

963	12	40.0	35	16	AAR74399	Parathyroid hormon
964	12	40.0	35	16	AAR74400	Parathyroid hormon
965	12	40.0	35	16	AAR74408	Parathyroid hormon
966	12	40.0	35	16	AAR74409	Parathyroid hormon
967	12	40.0	35	16	AAR74394	Parathyroid hormon
968	12	40.0	35	16	AAR74395	Parathyroid hormon
969	12	40.0	35	16	AAR74396	Parathyroid hormon
970	12	40.0	35	16	AAR74397	Parathyroid hormon
971	12	40.0	36	15	AAR58208	[A13,Q26,F27,D-F34
972	12	40.0	36	15	AAR58042	[L8,D10,K11,L18]-h
973	12	40.0	36	15	AAR58044	[L8,D10,K11,A17,L1
974	12	40.0	36	15	AAR58055	[L8,Q18]-hPTH(1-36
975	12	40.0	36	15	AAR58057	[L8,D10,A16,Q18]-h
976	12	40.0	36	15	AAR55820	[L8,D10,K11,Q18]-h
977	12	40.0	36	15	AAR55824	[L8,D10,K11,A16,Q1
978	12	40.0	36	15	AAR58027	[A1,A3,L8,Q18]-hPT
979	12	40.0	36	15	AAR58031	[L8,K11,Q18]-hPTH(
980	12	40.0	36	15	AAR58072	Isopropyl-[L8,D10,
981	12	40.0	36	15	AAR58074	[L8,Y18]-hPTH(1-36
982	11	36.7	30	22	AAB84834	Parathyroid hormon
983	11	36.7	30	22	AAB96905	Parathyroid hormon
984	11	36.7	32	12	AAR14726	Human parathyroid
985	11	36.7	32	22	AAB84835	Parathyroid hormon
986	11	36.7	32	22	AAB96906	Parathyroid hormon
987	11	36.7	34	15	AAR58045	[L8,Q16,D17,L18,R1
988	11	36.7	34	15	AAR58049	[L8,D10,K11,Q16,D1
989	11	36.7	34	15	AAR58056	[L8,D10,K11,A16,Q1
990	11	36.7	34	15	AAR58058	[L8,D10,K11,A16,Q1
991	11	36.7	34	15	AAR55818	[L8,A16,Q18,A19,T3
992	11	36.7	34	18	AAW08130	Human PTH derivati
993	11	36.7	34	18	AAW17960	Human PTH analogue
994	11	36.7	34	18	AAW17961	Human PTH analogue
995	11	36.7	34	18	AAW17962	Human PTH analogue
996	11	36.7	34	21	ABJ10757	Human parathyroid
997	11	36.7	34	21	ABJ10770	Human parathyroid
998	11	36.7	34	22	AAB84828	Parathyroid hormon
999	11	36.7	34	22	AAB96921	Parathyroid hormon
1000	11	36.7	35	16	AAR74506	Parathyroid hormon

ALIGNMENTS

RESULT 1

AAR88832

ID AAR88832 standard; peptide; 30 AA.

XX

AC AAR88832;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(1-30)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 30
 FT /note= "amidated"
 XX
 PN CA2126299-A.
 XX
 PD 21-DEC-1995.
 XX
 PF 20-JUN-1994; 94CA-2126299.
 XX
 PR 20-JUN-1994; 94CA-2126299.
 XX
 PA (WILL/) WILLICK G E.
 XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 1; Fig 5; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7.2e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 2

AAU73051

ID AAU73051 standard; Peptide; 30 AA.

XX

AC AAU73051;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #33.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7.2e-23;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 3

AAW42059

ID AAW42059 standard; peptide; 31 AA.

XX

AC AAW42059;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:14.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 22

FT /note= "Glu is bound to Lys at position 26 to form
FT a cyclic structure"

FT Modified-site 26

FT /note= "Lys is bound to Glu at position 22 to form
FT a cyclic structure"

FT Modified-site 31

FT /note= "amidated"

XX

PN W09805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution

PT - for treating osteoporosis and fractures, also method for screening

PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 41; Fig 21; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)

CC (1-31) peptide analogue. The present invention also describes a method

CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for
CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 30; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.4e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 4

AAW42051

ID AAW42051 standard; peptide; 31 AA.

XX

AC AAW42051;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:6.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 27

FT /note= "Lys is bound to Asp at position 30 to form
FT a cyclic structure"

FT Modified-site 30

FT /note= "Asp is bound to Lys at position 27 to form
FT a cyclic structure"

FT Modified-site 31

FT /note= "amidated"

XX

PN W09805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.
PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
PT - for treating osteoporosis and fractures, also method for screening
PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 33; Fig 10; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)
CC (1-31) peptide analogue. The present invention also describes a method
CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for
CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 30; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.4e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 5

AAAY02578

ID AAY02578 standard; peptide; 31 AA.

XX

AC AAY02578;

XX

DT 16-JUL-1999 (first entry)

XX

DE N-terminal 31 residues of human parathyroid hormone (hPTH).

XX

KW Human parathyroid hormone; hPTH; bone mass;
KW 3-(substituted phenoxy)benzo(b)thiophene compound;
KW bone loss treatment; osteoporosis.

XX

OS Homo sapiens.
 XX
 PN WO9918945-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 05-OCT-1998; 98WO-US20848.
 XX
 PR 14-OCT-1997; 97US-0061800.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Sato M;
 XX
 DR WPI; 1999-287871/24.
 XX
 PT Method of building bone mass by co-administration of a parathyroid
 PT hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound
 XX
 PS Claim 6; Page 39; 48pp; English.
 XX
 CC The present sequence represents a fragment of human parathyroid hormone
 CC (hPTH). hPTH and its fragments are used in the method of the invention.
 CC The specification describes a method for building bone mass, comprising
 CC coadministration of a parathyroid hormone with a 3-(substituted
 CC phenoxy)benzo(b)thiophene compound. The method is used for treatment
 CC of bone loss, e.g. in osteoporosis.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 30; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.4e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 6

AAB81080

ID AAB81080 standard; peptide; 31 AA.

XX

AC AAB81080;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human parathyroid hormone 1-31.

XX

KW Parathyroid hormone; PTH; blood calcium level regulator; osteopathic;

KW vulnerary; bone growth; bone healing; osteoporosis; fracture; human.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Modified-site 31

FT /note= "C-terminal amide"

XX
 PN WO200121643-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-CA01083.
 XX
 PR 22-SEP-1999; 99US-0406813.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Barbier J, Morley P, Whitfield J, Willick GE;
 XX
 DR WPI; 2001-308081/32.
 XX
 PT New human parathyroid hormone (hPTH) analog useful for stimulating bone
 PT growth, for restoring bone, for promotion of bone healing, and for
 PT treating osteoporosis and normal fractures -
 XX
 PS Disclosure; Fig 2; 34pp; English.
 XX
 CC Parathyroid hormone (PTH) is a major regulator of blood calcium levels,
 CC this invention relates to hPTH analogues, or their salts. Use of the
 CC analogues results in osteopathic and vulnerary activity. The hPTH
 CC analogues are useful for treating a warm-blooded animal for stimulating
 CC bone growth, for restoring bone, and for the promotion of bone healing
 CC during the treatment of osteoporosis and normal fractures. The present
 CC sequence represents human parathyroid hormone hPTH-NH2.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 30; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.4e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 7

AAB91097

ID AAB91097 standard; Peptide; 31 AA.

XX

AC AAB91097;

XX

DT 22-JUN-2001 (first entry)

XX

DE Parathyroid hormone (PTH) related peptide SEQ ID NO:271.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT -
 XX
 PS Disclosure; Page 281; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 31 AA;

 Query Match 100.0%; Score 30; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.4e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

 RESULT 8
 AAE23720
 ID AAE23720 standard; peptide; 31 AA.
 XX
 AC AAE23720;
 XX

DT 10-SEP-2002 (first entry)
 XX
 DE Human parathyroid hormone (hPTH) peptide (1-31).
 XX
 KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
 KW acne; actinic keratosis; alopecia; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200228420-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31082.
 XX
 PR 06-OCT-2000; 2000US-238134P.
 XX
 PA (HOLI/) HOLICK M F.
 XX
 PI Holick MF;
 XX
 DR WPI; 2002-452304/48.
 DR N-PSDB; AAD37995.
 XX
 PT Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein -
 XX
 PS Disclosure; Fig 8; 56pp; English.
 XX
 CC The invention relates to a method for regulating proliferation or
 CC enhancing differentiation of mammalian skin or hair cell. The method
 CC involves administering nucleic acids encoding peptides derived from
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
 CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
 CC healing, stimulating hair growth, maintaining hair growth, treating or
 CC preventing female or male pattern baldness, for treating chemotherapy
 CC induced alopecia and also for stimulating epidermal cell growth or
 CC hair follicle cell growth. The method is also used in gene therapy.
 CC The present sequence is hPTH peptide.
 XX
 SQ Sequence 31 AA;

 Query Match 100.0%; Score 30; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.4e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 9

AAU73039

ID AAU73039 standard; Peptide; 31 AA.

XX

AC AAU73039;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #21.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;

KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;

KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;

KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;

KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid

PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 26; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of

CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)

CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)

CC comprising PTH agonist optionally with a bone resorption inhibitor, such

CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,

CC oestrogens, oestrogen receptor modulators and tibolone is useful for

CC treating osteopenia. (I) is useful for therapeutic and prophylactic

CC purposes. Antagonists of PTH receptor are useful in treating primary and

CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,

CC particularly breast and prostate cancer, cachexia and anorexia,

CC osteopenia, including various forms of osteoporosis, Paget's disease of

CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with

CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 30; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.4e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

|||||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 10

AAU73177

ID AAU73177 standard; Peptide; 31 AA.

XX

AC AAU73177;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #159.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 63; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 30; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.4e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 11

AAU73176

ID AAU73176 standard; Peptide; 32 AA.

XX

AC AAU73176;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #158.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;

KW immunoglobulin G; IgG.
 XX
 OS Synthetic.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 63; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 30; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7.6e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 12

AAAY98018

ID AAY98018 standard; peptide; 33 AA.

XX

AC AAY98018;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human amino-terminal modified parathyroid hormone analogue # 9.

XX

KW Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;

KW signal transduction; osteoporosis; amino-terminal modification;

KW bone disease; parathyroid hormone receptor; osteopaenia;

KW hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Ser is desamino residue"

XX

PN WO200031137-A1.

XX

PD 02-JUN-2000.

XX

PF 23-NOV-1999; 99WO-US27656.

XX

PR 25-NOV-1998; 98US-0110152.

XX

PA (BRIN/) BRINGHURST F R.

PA (TAKA/) TAKASU H.

PA (GARD/) GARDELLA T J.

XX

PI Bringhurst FR, Takasu H, Gardella TJ;

XX

DR WPI; 2000-400045/34.

XX

PT New parathyroid hormone (PTH) analogs having one or more amino acid

PT substitutions that confer PTH-1/PTH-2 receptor agonist properties,

PT useful for treating old age osteoporosis and post-menopausal

PT osteoporosis -

XX

PS Disclosure; Page 65; 69pp; English.

XX

CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. The present
CC sequence is a human PTH peptide, with an amino-terminal modification
CC which results in effective activation of the PTH-2 receptor and therefore
CC downstream signalling. Aberrant PTH activity has been implicated in a
CC number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. This
CC peptide would be suitable for prophylaxis and treatment of the above

CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 14

AAP50377

ID AAP50377 standard; peptide; 34 AA.

XX

AC AAP50377;

XX

DT 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX

DE [Met(O)8,18]hPTH-(1-34).

XX

KW Human parathyroid hormone; calcium regulation.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Modified-site	8
----	---------------	---

FT		/label= oxidised methionine
----	--	-----------------------------

FT	Modified-site	18
----	---------------	----

FT		/label= oxidised methionine
----	--	-----------------------------

XX

PN JP59204159-A.

XX

PD 19-NOV-1984.

XX

PF 28-APR-1983; 83JP-0075607.

XX

PR 28-APR-1983; 83JP-0075607.

XX

PA (TOXN) TOYO JOZO KK.

XX

DR WPI; 1985-003560/01.

XX

PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 PT blood and decreases level in urine.

XX

PS Claim 1; Page 1; 3pp; Japanese.

XX
CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
CC decreases Ca in urine and increases P in urine by increasing cAMP in
CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
CC modified derivative only has the effect of lowering Ca levels in
CC urine and can be used when only this particular effect is required.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 15

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)

DT 06-JUL-1991 (first entry)

XX

DE Sequence of the first 34 AA residues of a parathyroid hormone
DE obtainable from a human or animal.

XX

KW Osteoporosis therapy.

XX

OS Homo sapiens/animal.

XX

PN EP197514-A.

XX

PD 15-OCT-1986.

XX

PF 03-APR-1986; 86EP-0104562.

XX

PR 04-APR-1985; 85US-0720018.

PR 05-DEC-1986; 86US-0939308.

PR 21-MAY-1987; 87US-0052383.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Potts JT, Neer RM, Slovik DM;

XX

DR WPI; 1986-273437/42.

XX

PT Compsn. and kits for increasing bone mass in osteoporosis -
PT contg. parathyroid hormone or fragment with hydroxylated
PT vitamin/D cpd. or calcium salt

XX

PS Claim 4; Page 24; 26pp; English.

XX
CC The peptide is used in a pharmaceutical compsn. together with a
CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.
CC (Updated on 25-MAR-2003 to correct PA field.)

XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 7; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 16

AAR07919

ID AAR07919 standard; protein; 34 AA.

XX

AC AAR07919;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

PN US4968669-A.

XX

PD 06-NOV-1990.

XX

PF 21-APR-1989; 89US-0341597.

XX

PR 21-APR-1989; 89US-0341597.

PR 09-MAY-1988; 88US-0191512.

XX

PA (MERI) MERCK & CO INC.

XX

PI Rosenblatt M, Chorev M;

XX

DR WPI; 1990-354642/47.

XX

PT New para:thyroid hormone analogues - which inhibit hormone
PT activity by binding receptors while not producing second
PT messenger molecules

XX

PS Claim 1; Column 8; 6pp; English.

XX

CC Peptide analogues have high affinity for PTH cell surface receptors,
CC but do not stimulate production of secondary messenger molecules.
CC They may be used in inhibition of PTH action, and in diagnosis and

CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
CC Analogues may also be used in treatment of tumours and other cells
CC overproducing peptide hormone-like substances, and immune diseases
CC eg. allergic inflammation and hyperactive lymphocytes.
CC Naturally occuring PTH levels may also be measured in vitro.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 17

AAR07922

ID AAR07922 standard; protein; 34 AA.

XX

AC AAR07922;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, Tyr34 hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

PN US4968669-A.

XX

PD 06-NOV-1990.

XX

PF 21-APR-1989; 89US-0341597.

XX

PR 21-APR-1989; 89US-0341597.

PR 09-MAY-1988; 88US-0191512.

XX

PA (MERI) MERCK & CO INC.

XX

PI Rosenblatt M, Chorev M;

XX

DR WPI; 1990-354642/47.

XX

PT New para:thyroid hormone analogues - which inhibit hormone

PT activity by binding receptors while not producing second

PT messenger molecules

XX

PS Claim 1; Column 8; 6pp; English.

XX

CC Peptide analogues have high affinity for PTH cell surface receptors,

CC but do not stimulate production of secondary messenger molecules.

CC They may be used in inhibition of PTH action, and in diagnosis and

CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.

CC Analogues may also be used in treatment of tumours and other cells

CC enhance cell proliferation (antagonist activity) for wound healing.
CC They are also applicable in the promotion of new hair growth or
CC stimulation of the rate of hair growth e.g. following chemotherapy
CC or for treating alopecia e.g. male pattern baldness.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 19

AAR41549

ID AAR41549 standard; protein; 34 AA.

XX

AC AAR41549;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ser3]hPTH (1-34)NH2.

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;

KW hypoparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 3

FT /note = "D-form residue"

FT Modified-site 34

FT /note = "C terminal is amidated"

XX

PN EP561412-A1.

XX

PD 22-SEP-1993.

XX

PF 18-MAR-1993; 93EP-0104500.

XX

PR 19-MAR-1992; 92JP-0063517.

PR 18-FEB-1993; 93JP-0029283.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Nakagawa S, Taketomi S;

XX

DR WPI; 1993-296712/38.

XX

PT New parathyroid hormone derivs. - used for the treatment of

PT osteoporosis hypoparathyroidism and hypertension

XX

PS Example 1; Page 17; 37pp; English.

CC proteases and a greater persistency of activity within the blood is
CC obtained. The proteins can be used to treat a number of bone and blood
CC disorders. This analogue was used as a test compound.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 21

AAR58291

ID AAR58291 standard; peptide; 34 AA.

XX

AC AAR58291;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Modified-site	26
FT		/label= Other
FT		/note= "Formyl-Lys."
FT	Modified-site	27
FT		/label= Other
FT		/note= "Formyl-Lys."
FT	Modified-site	34
FT		/note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 289; Page 47; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

 Query Match 100.0%; Score 30; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 22
 AAR58228
 ID AAR58228 standard; peptide; 34 AA.
 XX
 AC AAR58228;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [D-Asp30]-hPTH(1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 30
 FT /note= "D-form residue."
 FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX

PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 226; Page 45; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 23

AAR58232

ID AAR58232 standard; peptide; 34 AA.

XX

AC AAR58232;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys32]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 230; Page 45; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

 Query Match 100.0%; Score 30; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 24 .

AAR58181

ID AAR58181 standard; peptide; 34 AA.

XX

AC AAR58181;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Thr33, Ala34]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

XX

PS Example 179; Page 43; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.

XX

DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 1; Page 30; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 26

AAR58017

ID AAR58017 standard; peptide; 34 AA.
 XX
 AC AAR58017;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone(1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX

FH	Key	Location/Qualifiers
FT	Modified-site	26
FT		/note= "N-epsilon-Isopropyl-Lys"
FT	Modified-site	27
FT		/note= "N-epsilon-Isopropyl-Lys"
FT	Modified-site	34
FT		/note= "in amide form"

XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 2; Page 32; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 8e-23;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 27

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX

KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;
KW antiproliferative; tumor; psoriasis; docosaheptaenoic acid; DHA;
KW eicosapentaenoic acid; EPA; antitumor.

XX

OS Synthetic.

XX

PN WO9412530-A1.

XX
 PD 09-JUN-1994.
 XX
 PF 29-NOV-1993; 93WO-HU000065.
 XX
 PR 30-NOV-1992; 92US-0984293.
 XX
 PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
 PA (SYNT-) SYNTHETIC PEPTIDES INC.
 XX
 PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;
 PI Szederkenyi F, Vadasz Z;
 XX
 DR WPI; 1994-200194/24.
 XX
 PT New fatty acyl-peptide conjugates for inhibiting cell
 PT proliferation - more active than free peptide, partic. for
 PT treating tumours, virus-infected cells, psoriasis, etc.
 XX
 PS Disclosure; Fig. 1; 45pp; English.
 XX
 CC The peptides given in AAR55718-48 can each be conjugated through an
 CC amide linkage with a polyunsaturated fatty acid moiety, such as
 CC docosahexaenoic acid (DHA) or eicosapentanoic acid, to improve
 CC antiproliferative activity. The parathormone N-terminal fragment
 CC inhibits osteoblast proliferation.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 28
 AAR74521
 ID AAR74521 standard; Peptide; 34 AA.
 XX
 AC AAR74521;
 XX
 DT 25-MAR-2003 (updated)
 DT 04-DEC-1995 (first entry)
 XX
 DE Human parathyroid hormone (1-34).
 XX
 KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
 KW osteoporosis; hypercalcaemia; hyperparathroidism;
 KW metabolic bone disease; human; veterinary medicine;
 KW iontophoretic transdermal transport; recombinant E.coli.
 XX
 OS Homo sapiens.
 XX

PN WO9511988-A1.
 XX
 PD 04-MAY-1995.
 XX
 PF 25-OCT-1994; 94WO-US12205.
 XX
 PR 25-OCT-1993; 93US-0142551.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Oldenburg KR, Selick HE;
 XX
 DR WPI; 1995-178880/23.
 XX
 PT New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 XX
 PS Disclosure; Page 1; 109pp; English.
 XX
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (RPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport compared to wild type
 CC PTH and can be produced in high yield in recombinant E.coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 29

AAW99449

ID AAW99449 standard; peptide; 34 AA.

XX

AC AAW99449;

XX

DT 08-JUN-1999 (first entry)

XX

DE Human parathyroid hormone aal-34.

XX

KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
 KW spontaneous abortion; uterine contraction; human.

XX
 OS Homo sapiens.
 XX
 PN US5880093-A.
 XX
 PD 09-MAR-1999.
 XX
 PF 05-APR-1995; 95US-0411726.
 XX
 PR 28-SEP-1992; 92IT-MI02331.
 XX
 PA (BAGN/) BAGNOLI F.
 XX
 PI Bagnoli F;
 XX
 DR WPI; 1996-162392/17.
 XX
 PT Use of composition containing parathormone or fragments - for
 PT preventing premature birth or spontaneous abortion or for treating
 PT unwanted uterine contractions
 XX
 PS Disclosure; Column 7-8; 11pp; English.
 XX
 CC Peptides AAW99448-W99452 represent all or part of the parathyroid
 CC hormone (PTH; parathormone) sequence or related peptide. The peptides
 CC are used for preventing premature birth, spontaneous abortion or unwanted
 CC uterine contractions in a pregnant human patient.
 CC (Note: this patent is the first Major Country Equivalent to Italian
 CC Patent IT1255388).
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 30

AAR99978

ID AAR99978 standard; peptide; 34 AA.

XX

AC AAR99978;

XX

DT 30-APR-1997 (first entry)

XX

DE Human parathyroid hormone peptide fragment (1-34).

XX

KW cyclic parathyroid hormone fragment; calcium-regulating activity;

KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;

KW improved half life; calcium retention; bone.

XX

OS Synthetic.

XX

PN DE19508672-A1.
 XX
 PD 12-SEP-1996.
 XX
 PF 10-MAR-1995; 95DE-1008672.
 XX
 PR 10-MAR-1995; 95DE-1008672.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
 XX
 DR WPI; 1996-413519/42.
 XX
 PT Cyclic parathyroid hormone fragments with lactam bridge - have good
 PT in vivo half life and are useful for treating osteoporosis and
 PT preventing epidermal cell proliferation
 XX
 PS Disclosure; Page 9; 14pp; German.
 XX
 CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid
 CC sequence of h, b, p, r or cPTH(1-34), opt. extended by up to 4 amino
 CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
 CC the N-terminus, and are cyclised between positions 13 and 17. One of
 CC these positions is occupied by L- or D- Orn or Lys, and the other by L-
 CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
 CC treating osteoporosis and inhibit proliferation of epidermal cells (for
 CC treating psoriasis). The CPTH have an improved half life in vivo than
 CC known PTH fragments, increased mitogenicity and DNA-synthesising
 CC capacity, reduced catabolic, calcium-mobilising activity and increased
 CC activity for calcium retention and incorporation into bone. The
 CC present sequence is that of human PTH peptide fragment (1-34).
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 31
 AAR98951
 ID AAR98951 standard; peptide; 34 AA.
 XX
 AC AAR98951;
 XX
 DT 15-JAN-1997 (first entry)
 XX
 DE Target peptide (PTH(1-34)) used in fusion protein construct.
 XX
 KW Fusion protein construct; isolation; purification;
 KW growth hormone releasing factor; glucagon-like peptide 1;
 KW parathyroid hormone; inclusion body; carbonic anhydrase.

XX
 OS Synthetic.
 XX
 PN WO9617942-A1.
 XX
 PD 13-JUN-1996.
 XX
 PF 07-DEC-1995; 95WO-US15800.
 XX
 PR 07-DEC-1994; 94US-0350530.
 XX
 PA (BION-) BIONEBRASKA INC.
 XX
 PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;
 PI Partridge BE, Stout JS, Wagner FW;
 XX
 DR WPI; 1996-287186/29.
 XX
 PT Isolation and purificn of peptide(s) from fusion protein constructs
 PT - which include a carbonic anhydrase and a variable fused
 PT polypeptide
 XX
 PS Claim 18; Page 48; 67pp; English.
 XX
 CC A new method for the isolation and/or purification of a recombinant
 CC peptide employs a fusion protein construct (FPC) comprising a
 CC carbonic anhydrase and a variable fused polypeptide containing a
 CC target peptide. The method comprises precipitating either the FPC or
 CC a fragment of the FPC including the carbonic anhydrase. An
 CC alternative method of producing the peptide comprises expressing the
 CC FPC as part of an inclusion body. The target peptides of the FPC are
 CC derived from growth hormone releasing factor (GRF), glucagon-like
 CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
 CC corresponds to amino acids 1-34 of PTH.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 32

AAR98966

ID AAR98966 standard; Peptide; 34 AA.

XX

AC AAR98966;

XX

DT 02-DEC-1996 (first entry)

XX

DE PTH(1-34).

XX

KW PTH; parathyroid hormone; parathormone; C-amide;

KW C-amidated peptide; alpha-carboxamide; recombinant protein;
 KW fusion protein; transpeptidation.
 XX
 OS Not specified.
 XX
 PN WO9617941-A2.
 XX
 PD 13-JUN-1996.
 XX
 PF 07-DEC-1995; 95WO-US15799.
 XX
 PR 07-DEC-1994; 94US-0350528.
 XX
 PA (BION-) BIONEBRASKA INC.
 XX
 PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;
 PI Wagner FW;
 XX
 DR WPI; 1996-287185/29.
 XX
 PT Production of C-terminal alpha-carboxamidated peptide(s) - by
 PT cleavage and transpeptidation of recombinant multicopy peptide(s) or
 PT fusion constructs
 XX
 PS Claim 12; Page 70; 93pp; English.
 XX
 CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be
 CC produced as C-terminal amidated peptides utilising novel recombinant
 CC protein constructs (see also AAR98967-72) in which single or multiple
 CC copies of the peptide are linked by intraconnecting peptides that
 CC permit the construct to be selectively reacted to produce product
 CC peptides having a C-terminal alpha-carboxamide. Expression cassettes
 CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.
 CC of the recombinant proteins in transformed E. coli host cells.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 33

AAR88835

ID AAR88835 standard; peptide; 34 AA.

XX

AC AAR88835;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, cyclo-PTH(1-34)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;
 KW increased adenylyl cyclase activity; cAMPase; cyclic; bone loss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 10
 FT /note= "forms peptide bond with Lys at posn. 26"
 FT Modified-site 14
 FT /note= "forms peptide bond with Asp at posn. 30"
 FT Modified-site 26
 FT /note= "forms peptide bond with Asn at posn. 10"
 FT Modified-site 30
 FT /note= "forms peptide bond with His at posn. 14"
 FT Modified-site 34
 FT /note= "amidated"
 XX
 PN CA2126299-A.
 XX
 PD 21-DEC-1995.
 XX
 PF 20-JUN-1994; 94CA-2126299.
 XX
 PR 20-JUN-1994; 94CA-2126299.
 XX
 PA (WILL/) WILLICK G E.
 XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 3; Fig 8; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 34

AAW24273

ID AAW24273 standard; protein; 34 AA.

XX

AC AAW24273;

XX

DT 17-OCT-1997 (first entry)

XX

DE Wild type parathyroid hormone.

XX

KW Analogue; parathyroid hormone; PTH; hirudin; hirulog;
KW electrotransportability; alpha-helix; beta-sheet.

XX

OS Homo sapiens.

XX

PN WO9639423-A2.

XX

PD 12-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09647.

XX

PR 06-JUN-1995; 95US-0468275.

XX

PA (ALZA) ALZA CORP.

XX

PI Holladay LA, Oldenburg KR;

XX

DR WPI; 1997-043058/04.

XX

PT Prepn. of analogues of parent poly-peptide(s), esp. parathyroid
PT hormone and hirulog - which exhibit better or enhanced
PT electro-transportability through a body surface

XX

PS Claim 7; Fig 1A; 55pp; English.

XX

CC The sequences given in AAW24273-76 represent wildtype and analogues of
CC parathyroid hormone (PTH). The analogues exhibit better/enhanced
CC electrotransportability through a body surface, and are characterised
CC by substituting one or more amino acid residues of the parent
CC polypeptide to disrupt one or more alpha-helical and/or beta-sheet
CC segments of the parent polypeptide. An electrotransport device can
CC deliver the polypeptide analogue through a body surface by electro-
CC transport by including providing a therapeutically effective amount
CC of the polypeptide analogue in a donor reservoir of the electrotransport
CC device. The electrotransport flux of a polypeptide is increased by
CC reducing the potential of the polypeptide for forming alpha-helix or
CC beta-sheet segment.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 18; Length 34;

Best Local Similarity 100.0%; Pred. No. 8e-23;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 35

AAW19994

ID AAW19994 standard; peptide; 34 AA.

XX

AC AAW19994;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;

KW adenylate cyclase activity; bone growth; osteoporosis; fracture;

KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 13

FT /note= "joined via amide bond to residue 17"

FT Misc-difference 17

FT /note= "joined via amide bond to residue 13"

FT Misc-difference 34

FT /note= "amidated"

XX

PN WO9640193-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09674.

XX

PR 07-JUN-1995; 95US-0488105.

XX

PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX

PI Chorev M, Rosenblatt M;

XX

DR WPI; 1997-051884/05.

XX

PT New cyclic analogues of parathyroid hormone - having di:sulphide or
PT amide bond between residues 13 and 17 and/or between residues 26 and
PT 30, useful for treating osteoporosis and bone fractures

XX

PS Claim 4; Page -; 23pp; English.

XX

CC AAW19994 is a cyclised peptide derived from the N-terminal sequence
CC of human parathyroid hormone (PTH). The peptide is able to bind to
CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
CC PTH peptides stimulate bone growth and thus are useful in the
CC treatment of osteoporosis and bone fractures. Optionally they may
CC be administered concurrently with antiresorptive therapy (e.g.
CC bisphosphonate and calcitonin).

CC N.B. sequence not given in the specification, created from known
CC sequence of amino acids 1-34 of human PTH.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 36

AAW20000

ID AAW20000 standard; peptide; 34 AA.

XX

AC AAW20000;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;
KW adenylate cyclase activity; bone growth; osteoporosis; fracture;
KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 26

FT /note= "joined via amide bond to residue 30"

FT Misc-difference 30

FT /note= "joined via amide bond to residue 26"

FT Misc-difference 34

FT /note= "amidated"

XX

PN W09640193-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09674.

XX

PR 07-JUN-1995; 95US-0488105.

XX

PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX

PI Chorev M, Rosenblatt M;

XX

DR WPI; 1997-051884/05.

XX

PT New cyclic analogues of parathyroid hormone - having di:sulphide or
PT amide bond between residues 13 and 17 and/or between residues 26 and
PT 30, useful for treating osteoporosis and bone fractures

XX

PS Claim 6; Page -; 23pp; English.

XX

CC AAW20000 is a cyclised peptide derived from the N-terminal sequence
CC of human parathyroid hormone (PTH). The peptide is able to bind to
CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
CC PTH peptides stimulate bone growth and thus are useful in the

CC treatment of osteoporosis and bone fractures. Optionally they may
CC be administered concurrently with antiresorptive therapy (e.g.
CC bisphosphonate and calcitonin).
CC N.B. sequence not given in the specification, created from known
CC sequence of amino acids 1-34 of human PTH.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 37

AAW20006

ID AAW20006 standard; peptide; 34 AA.

XX

AC AAW20006;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;
KW adenylate cyclase activity; bone growth; osteoporosis; fracture;
KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Misc-difference 13

FT /note= "joined via amide bond to residue 17"

FT Misc-difference 17

FT /note= "joined via amide bond to residue 13"

FT Misc-difference 26

FT /note= "joined via amide bond to residue 30"

FT Misc-difference 30

FT /note= "joined via amide bond to residue 26"

FT Misc-difference 34

FT /note= "amidated"

XX

PN WO9640193-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09674.

XX

PR 07-JUN-1995; 95US-0488105.

XX

PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX

PI Chorev M, Rosenblatt M;

XX

DR WPI; 1997-051884/05.
 XX
 PT New cyclic analogues of parathyroid hormone - having di:sulphide or
 PT amide bond between residues 13 and 17 and/or between residues 26 and
 PT 30, useful for treating osteoporosis and bone fractures
 XX
 PS Claim 8; Page -; 23pp; English.
 XX
 CC AAW20006 is a cyclised peptide derived from the N-terminal sequence
 CC of human parathyroid hormone (PTH). The peptide is able to bind to
 CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
 CC PTH peptides stimulate bone growth and thus are useful in the
 CC treatment of osteoporosis and bone fractures. Optionally they may
 CC be administered concurrently with antiresorptive therapy (e.g.
 CC bisphosphonate and calcitonin).
 CC N.B. sequence not given in the specification, created from known
 CC sequence of amino acids 1-34 of human PTH.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 38

AAW17948

ID AAW17948 standard; peptide; 34 AA.

XX

AC AAW17948;

XX

DT 29-JUL-1997 (first entry)

XX

DE Human parathyroid hormone analogue [Cha31]hPTH(1-34)NH2.

XX

KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;

KW bone fracture.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 31

FT /label= OTHER

FT /note= "Cyclohexylalanine (Cha)"

FT Modified-site 34

FT /note= "In amide form"

XX

PN WO9702834-A1.

XX

PD 30-JAN-1997.

XX

PF 03-JUL-1996; 96WO-US11292.

XX
PR 29-MAR-1996; 96US-0626186.
PR 13-JUL-1995; 95US-0001105.
PR 06-SEP-1995; 95US-0003305.
XX
PA (BIOM-) BIOMEASURE INC.
XX
PI Dong ZX;
XX
DR WPI; 1997-118819/11.
XX
PT New variants of human parathyroid hormone 1-34 peptide - which
PT stimulate bone growth and are used for treatment of osteoporosis and
PT bone fracture
XX
PS Claim 7; Page -; 33pp; English.
XX
CC The present sequence is a specific example of a human parathyroid
CC hormone (hPTH) analogue from fragment 1-34 in which at least one
CC of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31
CC is cyclohexylalanine (Cha). In this example the Val residue at
CC position 31 of the wild-type has been substituted by Cha. The hPTH
CC analogues stimulate bone growth and so are useful in human or
CC veterinary medicine for treatment of osteoporosis and bone fracture,
CC optionally in conjunction with anti-resorptive therapy (bisphosphonates
CC and calcitonin).
CC N.B. The present sequence does not appear in the specification. It
CC corresponds to the known hPTH 1-34 fragment with the modifications
CC as stated in the claim.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 39
AAW17968
ID AAW17968 standard; peptide; 34 AA.
XX
AC AAW17968;
XX
DT 29-JUL-1997 (first entry)
XX
DE Human parathyroid hormone analogue [Nle31]hPTH(1-34)NH2.
XX
KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
KW bone fracture.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
 FT Modified-site 31
 FT /label= Nle
 FT Modified-site 34
 FT /note= "In amide form"
 XX
 PN WO9702834-A1.
 XX
 PD 30-JAN-1997.
 XX
 PF 03-JUL-1996; 96WO-US11292.
 XX
 PR 29-MAR-1996; 96US-0626186.
 PR 13-JUL-1995; 95US-0001105.
 PR 06-SEP-1995; 95US-0003305.
 XX
 PA (BIOM-) BIOMEASURE INC.
 XX
 PI Dong ZX;
 XX
 DR WPI; 1997-118819/11.
 XX
 PT New variants of human parathyroid hormone 1-34 peptide - which
 PT stimulate bone growth and are used for treatment of osteoporosis and
 PT bone fracture
 XX
 PS Claim 20; Page -; 33pp; English.
 XX
 CC The present sequence is a specific example of a human parathyroid
 CC hormone (hPTH) analogue from fragment 1-34 in which at least the amino
 CC acid residue at position 1 is alpha, beta-diaminopropionic acid,
 CC the amino acid residue at position 27 is homoarginine, or the amino acid
 CC residue at position 31 is norleucine. In this example the Val residue at
 CC position 31 in the wild-type has been substituted by Nle. The hPTH
 CC analogues stimulate bone growth and so are useful in human or
 CC veterinary medicine for treatment of osteoporosis and bone fracture,
 CC optionally in conjunction with anti-resorptive therapy (bisphosphonates
 CC and calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 CC corresponds to the known hPTH 1-34 fragment with the modifications
 CC as stated in the claim.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 30; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 40
 AAW17955
 ID AAW17955 standard; peptide; 34 AA.
 XX

AC AAW17955;
 XX
 DT 29-JUL-1997 (first entry)
 XX
 DE Human parathyroid hormone analogue [Aib34]hPTH(1-34)NH2.
 XX
 KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
 KW bone fracture.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 34
 FT /label= Aib
 FT /note= "In amide form"
 XX
 PN WO9702834-A1.
 XX
 PD 30-JAN-1997.
 XX
 PF 03-JUL-1996; 96WO-US11292.
 XX
 PR 29-MAR-1996; 96US-0626186.
 PR 13-JUL-1995; 95US-0001105.
 PR 06-SEP-1995; 95US-0003305.
 XX
 PA (BIOM-) BIOMEASURE INC.
 XX
 PI Dong ZX;
 XX
 DR WPI; 1997-118819/11.
 XX
 PT New variants of human parathyroid hormone 1-34 peptide - which
 PT stimulate bone growth and are used for treatment of osteoporosis and
 PT bone fracture
 XX
 PS Claim 11; Page -; 33pp; English.
 XX
 CC The present sequence is a specific example of a human parathyroid
 CC hormone (hPTH) analogue from fragment 1-34 in which at least one
 CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
 CC is alpha-aminoisobutyric acid (Aib). In this example the Phe residue
 CC at position 34 of the wild-type has been substituted by Aib. The hPTH
 CC analogues stimulate bone growth and so are useful in human or veterinary
 CC medicine for treatment of osteoporosis and bone fracture, optionally in
 CC conjunction with anti-resorptive therapy (bisphosphonates and
 CC calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 CC corresponds to the known hPTH 1-34 fragment with the modifications
 CC as stated in the claim.
 XX
 SQ Sequence 34 AA;

 Query Match 100.0%; Score 30; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

Search completed: January 14, 2004, 10:34:26
Job time : 30.6916 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 10.1869 Seconds
(without alignments)
124.604 Million cell updates/sec

Title: US-09-843-221A-166
Perfect score: 30
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	30	100.0	30	1	US-08-262-495C-5	Sequence 5, Appli
2	30	100.0	31	1	US-08-262-495C-3	Sequence 3, Appli
3	30	100.0	31	2	US-08-691-647C-1	Sequence 1, Appli
4	30	100.0	31	2	US-08-691-647C-6	Sequence 6, Appli
5	30	100.0	31	3	US-08-904-760B-1	Sequence 1, Appli
6	30	100.0	31	3	US-08-904-760B-6	Sequence 6, Appli
7	30	100.0	31	3	US-08-904-760B-14	Sequence 14, Appli
8	30	100.0	31	3	US-08-904-760B-32	Sequence 32, Appli
9	30	100.0	31	4	US-09-406-813-2	Sequence 2, Appli
10	30	100.0	31	4	US-09-536-785A-1	Sequence 1, Appli
11	30	100.0	31	4	US-09-536-785A-6	Sequence 6, Appli

12	30	100.0	31	4	US-09-536-785A-14	Sequence 14, Appl
13	30	100.0	31	4	US-09-536-785A-32	Sequence 32, Appl
14	30	100.0	33	4	US-09-447-800-9	Sequence 9, Appli
15	30	100.0	34	1	US-07-765-373-1	Sequence 1, Appli
16	30	100.0	34	1	US-08-033-099-1	Sequence 1, Appli
17	30	100.0	34	1	US-08-262-495C-1	Sequence 1, Appli
18	30	100.0	34	1	US-07-915-247A-1	Sequence 1, Appli
19	30	100.0	34	1	US-08-443-863-1	Sequence 1, Appli
20	30	100.0	34	1	US-08-448-070-1	Sequence 1, Appli
21	30	100.0	34	1	US-08-488-105-7	Sequence 7, Appli
22	30	100.0	34	1	US-08-468-275-6	Sequence 6, Appli
23	30	100.0	34	1	US-08-449-500-1	Sequence 1, Appli
24	30	100.0	34	1	US-08-449-317A-1	Sequence 1, Appli
25	30	100.0	34	2	US-08-142-551B-2	Sequence 2, Appli
26	30	100.0	34	2	US-08-477-022-1	Sequence 1, Appli
27	30	100.0	34	2	US-08-449-447-1	Sequence 1, Appli
28	30	100.0	34	2	US-08-835-231-13	Sequence 13, Appl
29	30	100.0	34	2	US-08-184-328-1	Sequence 1, Appli
30	30	100.0	34	2	US-08-411-726-2	Sequence 2, Appli
31	30	100.0	34	2	US-08-691-647C-5	Sequence 5, Appli
32	30	100.0	34	2	US-08-521-097-1	Sequence 1, Appli
33	30	100.0	34	3	US-09-044-536A-1	Sequence 1, Appli
34	30	100.0	34	3	US-08-904-760B-22	Sequence 22, Appl
35	30	100.0	34	3	US-08-903-497A-1	Sequence 1, Appli
36	30	100.0	34	3	US-09-108-661-13	Sequence 13, Appl
37	30	100.0	34	4	US-09-007-466-6	Sequence 6, Appli
38	30	100.0	34	4	US-09-406-813-1	Sequence 1, Appli
39	30	100.0	34	4	US-08-952-980B-6	Sequence 6, Appli
40	30	100.0	34	4	US-09-635-076-1	Sequence 1, Appli
41	30	100.0	34	4	US-09-228-990-1	Sequence 1, Appli
42	30	100.0	34	4	US-09-447-800-8	Sequence 8, Appli
43	30	100.0	34	4	US-09-536-785A-22	Sequence 22, Appl
44	30	100.0	34	4	US-09-442-989-26	Sequence 26, Appl
45	30	100.0	34	5	PCT-US95-15800-22	Sequence 22, Appl
46	30	100.0	35	1	US-08-256-363-3	Sequence 3, Appli
47	30	100.0	36	1	US-08-256-363-4	Sequence 4, Appli
48	30	100.0	37	1	US-08-440-117-1	Sequence 1, Appli
49	30	100.0	37	3	US-09-068-738A-16	Sequence 16, Appl
50	30	100.0	38	1	US-08-112-024-1	Sequence 1, Appli
51	30	100.0	38	1	US-08-232-849-1	Sequence 1, Appli
52	30	100.0	38	2	US-08-625-586-1	Sequence 1, Appli
53	30	100.0	38	3	US-09-128-401-1	Sequence 1, Appli
54	29	96.7	33	4	US-09-447-800-3	Sequence 3, Appli
55	29	96.7	33	4	US-09-447-800-6	Sequence 6, Appli
56	29	96.7	34	4	US-09-447-800-1	Sequence 1, Appli
57	29	96.7	34	4	US-09-447-800-2	Sequence 2, Appli
58	29	96.7	34	4	US-09-447-800-5	Sequence 5, Appli
59	29	96.7	36	1	US-08-112-024-2	Sequence 2, Appli
60	28	93.3	28	4	US-09-448-867-12	Sequence 12, Appl
61	28	93.3	33	1	US-08-256-363-1	Sequence 1, Appli
62	28	93.3	34	1	US-08-256-363-2	Sequence 2, Appli
63	27	90.0	28	4	US-09-448-867-8	Sequence 8, Appli
64	27	90.0	28	4	US-09-448-867-10	Sequence 10, Appl
65	27	90.0	34	4	US-09-449-632-24	Sequence 24, Appl
66	26	86.7	28	4	US-09-406-813-3	Sequence 3, Appli
67	26	86.7	29	4	US-09-406-813-4	Sequence 4, Appli
68	26	86.7	30	1	US-08-262-495C-6	Sequence 6, Appli

69	26	86.7	30	3	US-08-904-760B-7	Sequence 7, Appli
70	26	86.7	30	4	US-09-536-785A-7	Sequence 7, Appli
71	26	86.7	31	1	US-08-262-495C-4	Sequence 4, Appli
72	26	86.7	31	2	US-08-691-647C-2	Sequence 2, Appli
73	26	86.7	31	2	US-08-691-647C-3	Sequence 3, Appli
74	26	86.7	31	2	US-08-691-647C-4	Sequence 4, Appli
75	26	86.7	31	3	US-08-904-760B-2	Sequence 2, Appli
76	26	86.7	31	3	US-08-904-760B-3	Sequence 3, Appli
77	26	86.7	31	3	US-08-904-760B-4	Sequence 4, Appli
78	26	86.7	31	3	US-08-904-760B-5	Sequence 5, Appli
79	26	86.7	31	3	US-08-904-760B-8	Sequence 8, Appli
80	26	86.7	31	3	US-08-904-760B-11	Sequence 11, Appl
81	26	86.7	31	3	US-08-904-760B-12	Sequence 12, Appl
82	26	86.7	31	3	US-08-904-760B-15	Sequence 15, Appl
83	26	86.7	31	3	US-08-904-760B-16	Sequence 16, Appl
84	26	86.7	31	3	US-08-904-760B-17	Sequence 17, Appl
85	26	86.7	31	4	US-09-536-785A-2	Sequence 2, Appli
86	26	86.7	31	4	US-09-536-785A-3	Sequence 3, Appli
87	26	86.7	31	4	US-09-536-785A-4	Sequence 4, Appli
88	26	86.7	31	4	US-09-536-785A-5	Sequence 5, Appli
89	26	86.7	31	4	US-09-536-785A-8	Sequence 8, Appli
90	26	86.7	31	4	US-09-536-785A-11	Sequence 11, Appl
91	26	86.7	31	4	US-09-536-785A-12	Sequence 12, Appl
92	26	86.7	31	4	US-09-536-785A-15	Sequence 15, Appl
93	26	86.7	31	4	US-09-536-785A-16	Sequence 16, Appl
94	26	86.7	31	4	US-09-536-785A-17	Sequence 17, Appl
95	26	86.7	34	1	US-08-262-495C-2	Sequence 2, Appli
96	26	86.7	34	3	US-08-904-760B-9	Sequence 9, Appli
97	26	86.7	34	3	US-08-904-760B-10	Sequence 10, Appl
98	26	86.7	34	4	US-09-536-785A-9	Sequence 9, Appli
99	26	86.7	34	4	US-09-536-785A-10	Sequence 10, Appl
100	25	83.3	31	3	US-08-904-760B-21	Sequence 21, Appl
101	25	83.3	31	4	US-09-536-785A-21	Sequence 21, Appl
102	24	80.0	34	1	US-07-773-098-5	Sequence 5, Appli
103	24	80.0	34	1	US-07-773-098-6	Sequence 6, Appli
104	24	80.0	38	5	PCT-US95-15800-29	Sequence 29, Appl
105	21	70.0	31	3	US-08-904-760B-18	Sequence 18, Appl
106	21	70.0	31	3	US-08-904-760B-19	Sequence 19, Appl
107	21	70.0	31	3	US-08-904-760B-20	Sequence 20, Appl
108	21	70.0	31	4	US-09-536-785A-18	Sequence 18, Appl
109	21	70.0	31	4	US-09-536-785A-19	Sequence 19, Appl
110	21	70.0	31	4	US-09-536-785A-20	Sequence 20, Appl
111	20	66.7	34	3	US-09-044-536A-9	Sequence 9, Appli
112	20	66.7	34	3	US-09-044-536A-10	Sequence 10, Appl
113	20	66.7	34	3	US-09-044-536A-13	Sequence 13, Appl
114	20	66.7	34	3	US-09-044-536A-14	Sequence 14, Appl
115	20	66.7	34	3	US-09-044-536A-15	Sequence 15, Appl
116	20	66.7	34	4	US-08-952-980B-9	Sequence 9, Appli
117	19	63.3	34	3	US-09-044-536A-8	Sequence 8, Appli
118	19	63.3	34	3	US-09-044-536A-11	Sequence 11, Appl
119	19	63.3	34	3	US-09-044-536A-12	Sequence 12, Appl
120	18	60.0	28	4	US-09-448-867-6	Sequence 6, Appli
121	17	56.7	28	4	US-09-448-867-1	Sequence 1, Appli
122	17	56.7	28	4	US-09-448-867-2	Sequence 2, Appli
123	17	56.7	28	4	US-09-448-867-4	Sequence 4, Appli
124	17	56.7	34	3	US-09-044-536A-26	Sequence 26, Appl
125	16	53.3	28	4	US-09-406-813-6	Sequence 6, Appli

126	16	53.3	31	4	US-09-406-813-5	Sequence 5, Appli
127	16	53.3	34	1	US-08-488-105-1	Sequence 1, Appli
128	16	53.3	34	1	US-08-488-105-13	Sequence 13, Appl
129	16	53.3	34	3	US-09-044-536A-25	Sequence 25, Appl
130	16	53.3	34	3	US-08-903-497A-3	Sequence 3, Appli
131	16	53.3	34	4	US-09-635-076-3	Sequence 3, Appli
132	15	50.0	34	1	US-07-915-247A-3	Sequence 3, Appli
133	15	50.0	34	1	US-08-443-863-3	Sequence 3, Appli
134	15	50.0	34	1	US-08-448-070-3	Sequence 3, Appli
135	15	50.0	34	1	US-08-449-500-3	Sequence 3, Appli
136	15	50.0	34	1	US-08-449-317A-3	Sequence 3, Appli
137	15	50.0	34	2	US-08-477-022-3	Sequence 3, Appli
138	15	50.0	34	2	US-08-449-447-3	Sequence 3, Appli
139	15	50.0	34	2	US-08-184-328-3	Sequence 3, Appli
140	15	50.0	34	2	US-08-521-097-3	Sequence 3, Appli
141	15	50.0	34	3	US-09-044-536A-29	Sequence 29, Appl
142	14	46.7	34	1	US-07-915-247A-2	Sequence 2, Appli
143	14	46.7	34	1	US-08-443-863-2	Sequence 2, Appli
144	14	46.7	34	1	US-08-448-070-2	Sequence 2, Appli
145	14	46.7	34	1	US-08-488-105-2	Sequence 2, Appli
146	14	46.7	34	1	US-08-488-105-3	Sequence 3, Appli
147	14	46.7	34	1	US-08-488-105-8	Sequence 8, Appli
148	14	46.7	34	1	US-08-488-105-9	Sequence 9, Appli
149	14	46.7	34	1	US-08-488-105-15	Sequence 15, Appl
150	14	46.7	34	1	US-08-449-500-2	Sequence 2, Appli
151	14	46.7	34	1	US-08-449-317A-2	Sequence 2, Appli
152	14	46.7	34	2	US-08-477-022-2	Sequence 2, Appli
153	14	46.7	34	2	US-08-449-447-2	Sequence 2, Appli
154	14	46.7	34	2	US-08-184-328-2	Sequence 2, Appli
155	14	46.7	34	2	US-08-521-097-2	Sequence 2, Appli
156	14	46.7	34	3	US-09-044-536A-18	Sequence 18, Appl
157	14	46.7	34	3	US-09-044-536A-19	Sequence 19, Appl
158	14	46.7	34	3	US-08-903-497A-7	Sequence 7, Appli
159	14	46.7	34	4	US-09-635-076-7	Sequence 7, Appli
160	13	43.3	30	3	US-08-904-760B-33	Sequence 33, Appl
161	13	43.3	30	3	US-08-904-760B-34	Sequence 34, Appl
162	13	43.3	30	3	US-08-904-760B-35	Sequence 35, Appl
163	13	43.3	30	4	US-09-536-785A-33	Sequence 33, Appl
164	13	43.3	30	4	US-09-536-785A-34	Sequence 34, Appl
165	13	43.3	30	4	US-09-536-785A-35	Sequence 35, Appl
166	13	43.3	34	1	US-08-488-105-14	Sequence 14, Appl
167	13	43.3	34	3	US-09-044-536A-16	Sequence 16, Appl
168	13	43.3	34	3	US-09-044-536A-17	Sequence 17, Appl
169	12	40.0	34	1	US-08-049-402-2	Sequence 2, Appli
170	12	40.0	34	1	US-08-488-105-4	Sequence 4, Appli
171	12	40.0	34	1	US-08-488-105-6	Sequence 6, Appli
172	12	40.0	34	1	US-08-488-105-10	Sequence 10, Appl
173	12	40.0	34	1	US-08-488-105-11	Sequence 11, Appl
174	12	40.0	34	1	US-08-488-105-16	Sequence 16, Appl
175	12	40.0	34	1	US-08-488-105-18	Sequence 18, Appl
176	12	40.0	34	1	US-08-526-987-2	Sequence 2, Appli
177	12	40.0	34	1	US-08-449-500-79	Sequence 79, Appl
178	12	40.0	34	1	US-08-449-317A-79	Sequence 79, Appl
179	12	40.0	34	2	US-08-142-551B-3	Sequence 3, Appli
180	12	40.0	34	2	US-08-477-022-79	Sequence 79, Appl
181	12	40.0	34	2	US-08-449-447-79	Sequence 79, Appl
182	12	40.0	34	2	US-08-184-328-79	Sequence 79, Appl

183	12	40.0	34	2	US-08-521-097-79	Sequence 79, Appl
184	12	40.0	34	3	US-08-903-497A-4	Sequence 4, Appli
185	12	40.0	34	4	US-09-635-076-4	Sequence 4, Appli
186	12	40.0	35	2	US-08-142-551B-4	Sequence 4, Appli
187	12	40.0	35	2	US-08-142-551B-5	Sequence 5, Appli
188	12	40.0	35	2	US-08-142-551B-7	Sequence 7, Appli
189	12	40.0	35	2	US-08-142-551B-11	Sequence 11, Appl
190	12	40.0	35	2	US-08-142-551B-12	Sequence 12, Appl
191	12	40.0	35	2	US-08-142-551B-13	Sequence 13, Appl
192	12	40.0	35	2	US-08-142-551B-14	Sequence 14, Appl
193	12	40.0	35	2	US-08-142-551B-15	Sequence 15, Appl
194	12	40.0	35	2	US-08-142-551B-16	Sequence 16, Appl
195	12	40.0	35	2	US-08-142-551B-17	Sequence 17, Appl
196	12	40.0	35	2	US-08-142-551B-18	Sequence 18, Appl
197	12	40.0	35	2	US-08-142-551B-19	Sequence 19, Appl
198	12	40.0	35	2	US-08-142-551B-20	Sequence 20, Appl
199	12	40.0	35	2	US-08-142-551B-21	Sequence 21, Appl
200	12	40.0	35	2	US-08-142-551B-22	Sequence 22, Appl
201	12	40.0	35	2	US-08-142-551B-23	Sequence 23, Appl
202	12	40.0	35	2	US-08-142-551B-24	Sequence 24, Appl
203	12	40.0	35	2	US-08-142-551B-25	Sequence 25, Appl
204	12	40.0	35	2	US-08-142-551B-26	Sequence 26, Appl
205	12	40.0	35	2	US-08-142-551B-27	Sequence 27, Appl
206	12	40.0	35	2	US-08-142-551B-28	Sequence 28, Appl
207	12	40.0	35	2	US-08-142-551B-29	Sequence 29, Appl
208	12	40.0	35	2	US-08-142-551B-30	Sequence 30, Appl
209	12	40.0	35	2	US-08-142-551B-31	Sequence 31, Appl
210	12	40.0	35	2	US-08-142-551B-32	Sequence 32, Appl
211	12	40.0	35	2	US-08-142-551B-33	Sequence 33, Appl
212	12	40.0	35	2	US-08-142-551B-34	Sequence 34, Appl
213	12	40.0	35	2	US-08-142-551B-35	Sequence 35, Appl
214	12	40.0	35	2	US-08-142-551B-36	Sequence 36, Appl
215	12	40.0	35	2	US-08-142-551B-37	Sequence 37, Appl
216	12	40.0	35	2	US-08-142-551B-38	Sequence 38, Appl
217	12	40.0	35	2	US-08-142-551B-39	Sequence 39, Appl
218	12	40.0	35	2	US-08-142-551B-40	Sequence 40, Appl
219	12	40.0	35	2	US-08-142-551B-41	Sequence 41, Appl
220	12	40.0	35	2	US-08-142-551B-42	Sequence 42, Appl
221	12	40.0	35	2	US-08-142-551B-43	Sequence 43, Appl
222	12	40.0	35	2	US-08-142-551B-44	Sequence 44, Appl
223	12	40.0	35	2	US-08-142-551B-45	Sequence 45, Appl
224	12	40.0	35	2	US-08-142-551B-46	Sequence 46, Appl
225	12	40.0	35	2	US-08-142-551B-47	Sequence 47, Appl
226	12	40.0	35	2	US-08-142-551B-48	Sequence 48, Appl
227	12	40.0	35	2	US-08-142-551B-49	Sequence 49, Appl
228	12	40.0	35	2	US-08-142-551B-50	Sequence 50, Appl
229	12	40.0	35	2	US-08-142-551B-51	Sequence 51, Appl
230	12	40.0	35	2	US-08-142-551B-52	Sequence 52, Appl
231	12	40.0	35	2	US-08-142-551B-53	Sequence 53, Appl
232	12	40.0	35	2	US-08-142-551B-54	Sequence 54, Appl
233	12	40.0	35	2	US-08-142-551B-55	Sequence 55, Appl
234	12	40.0	35	2	US-08-142-551B-56	Sequence 56, Appl
235	12	40.0	35	2	US-08-142-551B-57	Sequence 57, Appl
236	12	40.0	35	2	US-08-142-551B-58	Sequence 58, Appl
237	12	40.0	35	2	US-08-142-551B-59	Sequence 59, Appl
238	12	40.0	35	2	US-08-142-551B-60	Sequence 60, Appl
239	12	40.0	35	2	US-08-142-551B-61	Sequence 61, Appl

240	12	40.0	35	2	US-08-142-551B-62	Sequence 62, Appl
241	12	40.0	35	2	US-08-142-551B-63	Sequence 63, Appl
242	12	40.0	35	2	US-08-142-551B-64	Sequence 64, Appl
243	12	40.0	35	2	US-08-142-551B-65	Sequence 65, Appl
244	12	40.0	35	2	US-08-142-551B-66	Sequence 66, Appl
245	12	40.0	35	2	US-08-142-551B-67	Sequence 67, Appl
246	12	40.0	35	2	US-08-142-551B-68	Sequence 68, Appl
247	12	40.0	35	2	US-08-142-551B-70	Sequence 70, Appl
248	12	40.0	35	2	US-08-142-551B-73	Sequence 73, Appl
249	12	40.0	35	2	US-08-142-551B-80	Sequence 80, Appl
250	12	40.0	35	2	US-08-142-551B-90	Sequence 90, Appl
251	12	40.0	35	2	US-08-142-551B-94	Sequence 94, Appl
252	12	40.0	35	2	US-08-142-551B-107	Sequence 107, App
253	12	40.0	35	2	US-08-142-551B-108	Sequence 108, App
254	12	40.0	35	2	US-08-142-551B-109	Sequence 109, App
255	12	40.0	35	2	US-08-142-551B-110	Sequence 110, App
256	12	40.0	35	2	US-08-142-551B-111	Sequence 111, App
257	12	40.0	35	2	US-08-142-551B-112	Sequence 112, App
258	12	40.0	35	2	US-08-142-551B-113	Sequence 113, App
259	12	40.0	35	2	US-08-142-551B-114	Sequence 114, App
260	12	40.0	35	2	US-08-142-551B-115	Sequence 115, App
261	12	40.0	35	2	US-08-142-551B-116	Sequence 116, App
262	12	40.0	35	2	US-08-142-551B-117	Sequence 117, App
263	12	40.0	35	2	US-08-142-551B-118	Sequence 118, App
264	11	36.7	34	3	US-09-044-536A-27	Sequence 27, Appl
265	11	36.7	35	2	US-08-142-551B-69	Sequence 69, Appl
266	11	36.7	35	2	US-08-142-551B-71	Sequence 71, Appl
267	11	36.7	35	2	US-08-142-551B-104	Sequence 104, App
268	11	36.7	35	2	US-08-142-551B-105	Sequence 105, App
269	11	36.7	35	2	US-08-142-551B-106	Sequence 106, App
270	11	36.7	35	2	US-08-142-551B-122	Sequence 122, App
271	10	33.3	34	1	US-08-033-099-2	Sequence 2, Appli
272	10	33.3	34	3	US-09-044-536A-20	Sequence 20, Appl
273	10	33.3	34	3	US-09-044-536A-21	Sequence 21, Appl
274	10	33.3	34	3	US-09-044-536A-22	Sequence 22, Appl
275	10	33.3	34	3	US-09-044-536A-24	Sequence 24, Appl
276	10	33.3	34	3	US-09-044-536A-28	Sequence 28, Appl
277	10	33.3	35	2	US-08-142-551B-72	Sequence 72, Appl
278	10	33.3	35	2	US-08-142-551B-74	Sequence 74, Appl
279	10	33.3	35	2	US-08-142-551B-75	Sequence 75, Appl
280	10	33.3	35	2	US-08-142-551B-101	Sequence 101, App
281	10	33.3	35	2	US-08-142-551B-102	Sequence 102, App
282	10	33.3	35	2	US-08-142-551B-103	Sequence 103, App
283	10	33.3	35	2	US-08-142-551B-120	Sequence 120, App
284	9	30.0	28	4	US-09-228-990-54	Sequence 54, Appl
285	9	30.0	28	4	US-09-228-990-62	Sequence 62, Appl
286	9	30.0	28	4	US-09-228-990-65	Sequence 65, Appl
287	9	30.0	28	4	US-09-228-990-79	Sequence 79, Appl
288	9	30.0	28	4	US-09-442-989-22	Sequence 22, Appl
289	9	30.0	28	4	US-09-442-989-25	Sequence 25, Appl
290	9	30.0	29	4	US-09-406-813-8	Sequence 8, Appli
291	9	30.0	29	4	US-09-228-990-53	Sequence 53, Appl
292	9	30.0	29	4	US-09-228-990-63	Sequence 63, Appl
293	9	30.0	30	4	US-09-228-990-52	Sequence 52, Appl
294	9	30.0	30	4	US-09-228-990-64	Sequence 64, Appl
295	9	30.0	31	3	US-08-904-760B-13	Sequence 13, Appl
296	9	30.0	31	4	US-09-228-990-3	Sequence 3, Appli

297	9	30.0	31	4	US-09-228-990-4	Sequence 4, Appli
298	9	30.0	31	4	US-09-228-990-5	Sequence 5, Appli
299	9	30.0	31	4	US-09-228-990-6	Sequence 6, Appli
300	9	30.0	31	4	US-09-228-990-7	Sequence 7, Appli
301	9	30.0	31	4	US-09-228-990-8	Sequence 8, Appli
302	9	30.0	31	4	US-09-228-990-9	Sequence 9, Appli
303	9	30.0	31	4	US-09-228-990-10	Sequence 10, Appl
304	9	30.0	31	4	US-09-228-990-20	Sequence 20, Appl
305	9	30.0	31	4	US-09-228-990-21	Sequence 21, Appl
306	9	30.0	31	4	US-09-228-990-22	Sequence 22, Appl
307	9	30.0	31	4	US-09-228-990-23	Sequence 23, Appl
308	9	30.0	31	4	US-09-228-990-24	Sequence 24, Appl
309	9	30.0	31	4	US-09-228-990-25	Sequence 25, Appl
310	9	30.0	31	4	US-09-228-990-26	Sequence 26, Appl
311	9	30.0	31	4	US-09-228-990-27	Sequence 27, Appl
312	9	30.0	31	4	US-09-228-990-36	Sequence 36, Appl
313	9	30.0	31	4	US-09-228-990-37	Sequence 37, Appl
314	9	30.0	31	4	US-09-228-990-38	Sequence 38, Appl
315	9	30.0	31	4	US-09-228-990-39	Sequence 39, Appl
316	9	30.0	31	4	US-09-228-990-47	Sequence 47, Appl
317	9	30.0	31	4	US-09-228-990-48	Sequence 48, Appl
318	9	30.0	31	4	US-09-228-990-49	Sequence 49, Appl
319	9	30.0	31	4	US-09-228-990-50	Sequence 50, Appl
320	9	30.0	31	4	US-09-228-990-51	Sequence 51, Appl
321	9	30.0	31	4	US-09-228-990-69	Sequence 69, Appl
322	9	30.0	31	4	US-09-228-990-70	Sequence 70, Appl
323	9	30.0	31	4	US-09-228-990-74	Sequence 74, Appl
324	9	30.0	31	4	US-09-228-990-81	Sequence 81, Appl
325	9	30.0	31	4	US-09-228-990-82	Sequence 82, Appl
326	9	30.0	31	4	US-09-228-990-83	Sequence 83, Appl
327	9	30.0	31	4	US-09-228-990-84	Sequence 84, Appl
328	9	30.0	31	4	US-09-228-990-85	Sequence 85, Appl
329	9	30.0	31	4	US-09-536-785A-13	Sequence 13, Appl
330	9	30.0	31	4	US-09-442-989-1	Sequence 1, Appli
331	9	30.0	31	4	US-09-442-989-2	Sequence 2, Appli
332	9	30.0	31	4	US-09-442-989-3	Sequence 3, Appli
333	9	30.0	31	4	US-09-442-989-4	Sequence 4, Appli
334	9	30.0	31	4	US-09-442-989-5	Sequence 5, Appli
335	9	30.0	31	4	US-09-442-989-6	Sequence 6, Appli
336	9	30.0	31	4	US-09-442-989-7	Sequence 7, Appli
337	9	30.0	31	4	US-09-442-989-8	Sequence 8, Appli
338	9	30.0	31	4	US-09-442-989-17	Sequence 17, Appl
339	9	30.0	31	4	US-09-442-989-32	Sequence 32, Appl
340	9	30.0	34	3	US-09-044-536A-2	Sequence 2, Appli
341	9	30.0	34	3	US-09-044-536A-23	Sequence 23, Appl
342	9	30.0	34	3	US-08-903-497A-5	Sequence 5, Appli
343	9	30.0	34	4	US-09-635-076-5	Sequence 5, Appli
344	9	30.0	34	4	US-09-228-990-46	Sequence 46, Appl
345	9	30.0	34	4	US-09-442-989-18	Sequence 18, Appl
346	9	30.0	34	4	US-09-442-989-46	Sequence 46, Appl
347	9	30.0	35	2	US-08-142-551B-76	Sequence 76, Appl
348	9	30.0	35	2	US-08-142-551B-77	Sequence 77, Appl
349	9	30.0	35	2	US-08-142-551B-78	Sequence 78, Appl
350	9	30.0	35	2	US-08-142-551B-79	Sequence 79, Appl
351	9	30.0	35	2	US-08-142-551B-81	Sequence 81, Appl
352	9	30.0	35	2	US-08-142-551B-82	Sequence 82, Appl
353	9	30.0	35	2	US-08-142-551B-83	Sequence 83, Appl

354	9	30.0	35	2	US-08-142-551B-84	Sequence 84, Appl
355	9	30.0	35	2	US-08-142-551B-85	Sequence 85, Appl
356	9	30.0	35	2	US-08-142-551B-86	Sequence 86, Appl
357	9	30.0	35	2	US-08-142-551B-87	Sequence 87, Appl
358	9	30.0	35	2	US-08-142-551B-88	Sequence 88, Appl
359	9	30.0	35	2	US-08-142-551B-89	Sequence 89, Appl
360	9	30.0	35	2	US-08-142-551B-91	Sequence 91, Appl
361	9	30.0	35	2	US-08-142-551B-92	Sequence 92, Appl
362	9	30.0	35	2	US-08-142-551B-93	Sequence 93, Appl
363	9	30.0	35	2	US-08-142-551B-95	Sequence 95, Appl
364	9	30.0	35	2	US-08-142-551B-96	Sequence 96, Appl
365	9	30.0	35	2	US-08-142-551B-97	Sequence 97, Appl
366	9	30.0	35	2	US-08-142-551B-98	Sequence 98, Appl
367	9	30.0	35	2	US-08-142-551B-99	Sequence 99, Appl
368	9	30.0	35	2	US-08-142-551B-100	Sequence 100, App
369	9	30.0	35	2	US-08-142-551B-123	Sequence 123, App
370	9	30.0	35	3	US-09-044-536A-30	Sequence 30, Appl
371	9	30.0	36	3	US-09-044-536A-31	Sequence 31, Appl
372	9	30.0	37	3	US-09-044-536A-32	Sequence 32, Appl
373	9	30.0	38	3	US-09-044-536A-33	Sequence 33, Appl
374	9	30.0	39	3	US-09-044-536A-34	Sequence 34, Appl
375	9	30.0	40	3	US-09-044-536A-35	Sequence 35, Appl
376	8	26.7	28	4	US-09-228-990-78	Sequence 78, Appl
377	8	26.7	28	4	US-09-442-989-24	Sequence 24, Appl
378	8	26.7	29	1	US-07-778-926-6	Sequence 6, Appli
379	8	26.7	30	1	US-07-778-926-10	Sequence 10, Appl
380	8	26.7	31	1	US-07-778-926-14	Sequence 14, Appl
381	8	26.7	31	4	US-09-228-990-11	Sequence 11, Appl
382	8	26.7	31	4	US-09-228-990-19	Sequence 19, Appl
383	8	26.7	31	4	US-09-228-990-28	Sequence 28, Appl
384	8	26.7	31	4	US-09-228-990-35	Sequence 35, Appl
385	8	26.7	31	4	US-09-228-990-40	Sequence 40, Appl
386	8	26.7	31	4	US-09-228-990-45	Sequence 45, Appl
387	8	26.7	31	4	US-09-228-990-66	Sequence 66, Appl
388	8	26.7	31	4	US-09-228-990-67	Sequence 67, Appl
389	8	26.7	31	4	US-09-228-990-68	Sequence 68, Appl
390	8	26.7	31	4	US-09-228-990-73	Sequence 73, Appl
391	8	26.7	31	4	US-09-228-990-76	Sequence 76, Appl
392	8	26.7	31	4	US-09-228-990-80	Sequence 80, Appl
393	8	26.7	31	4	US-09-442-989-16	Sequence 16, Appl
394	8	26.7	32	1	US-07-778-926-18	Sequence 18, Appl
395	8	26.7	33	1	US-07-778-926-7	Sequence 7, Appli
396	8	26.7	34	1	US-07-778-926-11	Sequence 11, Appl
397	8	26.7	34	1	US-07-773-098-3	Sequence 3, Appli
398	8	26.7	34	1	US-07-773-098-4	Sequence 4, Appli
399	8	26.7	34	1	US-08-488-105-5	Sequence 5, Appli
400	8	26.7	34	1	US-08-488-105-12	Sequence 12, Appl
401	8	26.7	34	1	US-08-488-105-17	Sequence 17, Appl
402	8	26.7	34	1	US-08-449-500-61	Sequence 61, Appl
403	8	26.7	34	1	US-08-449-317A-61	Sequence 61, Appl
404	8	26.7	34	2	US-08-477-022-61	Sequence 61, Appl
405	8	26.7	34	2	US-08-449-447-61	Sequence 61, Appl
406	8	26.7	34	2	US-08-184-328-61	Sequence 61, Appl
407	8	26.7	34	2	US-08-521-097-61	Sequence 61, Appl
408	8	26.7	34	4	US-09-228-990-75	Sequence 75, Appl
409	8	26.7	34	4	US-09-449-632-22	Sequence 22, Appl
410	8	26.7	34	4	US-09-442-989-19	Sequence 19, Appl

411	8	26.7	35	1	US-07-778-926-15	Sequence 15, Appl
412	8	26.7	35	2	US-08-142-551B-121	Sequence 121, App
413	8	26.7	36	1	US-07-778-926-19	Sequence 19, Appl
414	8	26.7	37	1	US-07-778-926-8	Sequence 8, Appli
415	8	26.7	38	1	US-07-778-926-12	Sequence 12, Appl
416	8	26.7	39	1	US-07-778-926-16	Sequence 16, Appl
417	8	26.7	40	1	US-07-778-926-20	Sequence 20, Appl
418	7	23.3	28	1	US-07-778-926-2	Sequence 2, Appli
419	7	23.3	31	4	US-09-406-813-9	Sequence 9, Appli
420	7	23.3	31	4	US-09-228-990-12	Sequence 12, Appl
421	7	23.3	31	4	US-09-228-990-18	Sequence 18, Appl
422	7	23.3	31	4	US-09-228-990-29	Sequence 29, Appl
423	7	23.3	31	4	US-09-228-990-34	Sequence 34, Appl
424	7	23.3	31	4	US-09-228-990-41	Sequence 41, Appl
425	7	23.3	31	4	US-09-228-990-44	Sequence 44, Appl
426	7	23.3	31	4	US-09-442-989-9	Sequence 9, Appli
427	7	23.3	31	4	US-09-442-989-15	Sequence 15, Appl
428	7	23.3	32	1	US-07-778-926-3	Sequence 3, Appli
429	7	23.3	32	1	US-08-305-799A-1	Sequence 1, Appli
430	7	23.3	32	1	US-08-305-799A-2	Sequence 2, Appli
431	7	23.3	34	1	US-07-915-247A-23	Sequence 23, Appl
432	7	23.3	34	1	US-07-915-247A-24	Sequence 24, Appl
433	7	23.3	34	1	US-08-443-863-23	Sequence 23, Appl
434	7	23.3	34	1	US-08-443-863-24	Sequence 24, Appl
435	7	23.3	34	1	US-08-448-070-23	Sequence 23, Appl
436	7	23.3	34	1	US-08-448-070-24	Sequence 24, Appl
437	7	23.3	34	1	US-08-468-275-7	Sequence 7, Appli
438	7	23.3	34	1	US-08-468-275-8	Sequence 8, Appli
439	7	23.3	34	1	US-08-449-500-23	Sequence 23, Appl
440	7	23.3	34	1	US-08-449-500-24	Sequence 24, Appl
441	7	23.3	34	1	US-08-449-500-35	Sequence 35, Appl
442	7	23.3	34	1	US-08-449-500-36	Sequence 36, Appl
443	7	23.3	34	1	US-08-449-317A-23	Sequence 23, Appl
444	7	23.3	34	1	US-08-449-317A-24	Sequence 24, Appl
445	7	23.3	34	1	US-08-449-317A-35	Sequence 35, Appl
446	7	23.3	34	1	US-08-449-317A-36	Sequence 36, Appl
447	7	23.3	34	2	US-08-477-022-23	Sequence 23, Appl
448	7	23.3	34	2	US-08-477-022-24	Sequence 24, Appl
449	7	23.3	34	2	US-08-477-022-35	Sequence 35, Appl
450	7	23.3	34	2	US-08-477-022-36	Sequence 36, Appl
451	7	23.3	34	2	US-08-449-447-23	Sequence 23, Appl
452	7	23.3	34	2	US-08-449-447-24	Sequence 24, Appl
453	7	23.3	34	2	US-08-449-447-35	Sequence 35, Appl
454	7	23.3	34	2	US-08-449-447-36	Sequence 36, Appl
455	7	23.3	34	2	US-08-184-328-23	Sequence 23, Appl
456	7	23.3	34	2	US-08-184-328-24	Sequence 24, Appl
457	7	23.3	34	2	US-08-184-328-35	Sequence 35, Appl
458	7	23.3	34	2	US-08-184-328-36	Sequence 36, Appl
459	7	23.3	34	2	US-08-521-097-23	Sequence 23, Appl
460	7	23.3	34	2	US-08-521-097-24	Sequence 24, Appl
461	7	23.3	34	2	US-08-521-097-35	Sequence 35, Appl
462	7	23.3	34	2	US-08-521-097-36	Sequence 36, Appl
463	7	23.3	34	3	US-08-903-497A-6	Sequence 6, Appli
464	7	23.3	34	4	US-09-007-466-7	Sequence 7, Appli
465	7	23.3	34	4	US-09-007-466-8	Sequence 8, Appli
466	7	23.3	34	4	US-09-635-076-6	Sequence 6, Appli
467	7	23.3	35	2	US-08-142-551B-10	Sequence 10, Appl

468	7	23.3	35	2	US-08-142-551B-124	Sequence 124, App
469	7	23.3	35	4	US-08-952-980B-7	Sequence 7, Appli
470	7	23.3	35	4	US-08-952-980B-8	Sequence 8, Appli
471	7	23.3	36	1	US-07-778-926-4	Sequence 4, Appli
472	6	20.0	30	4	US-09-536-785A-23	Sequence 23, Appl
473	6	20.0	31	3	US-08-904-760B-23	Sequence 23, Appl
474	6	20.0	31	4	US-09-406-813-7	Sequence 7, Appli
475	6	20.0	31	4	US-09-228-990-13	Sequence 13, Appl
476	6	20.0	31	4	US-09-228-990-14	Sequence 14, Appl
477	6	20.0	31	4	US-09-228-990-15	Sequence 15, Appl
478	6	20.0	31	4	US-09-228-990-16	Sequence 16, Appl
479	6	20.0	31	4	US-09-228-990-17	Sequence 17, Appl
480	6	20.0	31	4	US-09-228-990-30	Sequence 30, Appl
481	6	20.0	31	4	US-09-228-990-31	Sequence 31, Appl
482	6	20.0	31	4	US-09-228-990-32	Sequence 32, Appl
483	6	20.0	31	4	US-09-228-990-33	Sequence 33, Appl
484	6	20.0	31	4	US-09-228-990-42	Sequence 42, Appl
485	6	20.0	31	4	US-09-228-990-43	Sequence 43, Appl
486	6	20.0	31	4	US-09-228-990-86	Sequence 86, Appl
487	6	20.0	31	4	US-09-228-990-87	Sequence 87, Appl
488	6	20.0	31	4	US-09-228-990-88	Sequence 88, Appl
489	6	20.0	31	4	US-09-536-785A-36	Sequence 36, Appl
490	6	20.0	31	4	US-09-442-989-10	Sequence 10, Appl
491	6	20.0	31	4	US-09-442-989-11	Sequence 11, Appl
492	6	20.0	31	4	US-09-442-989-12	Sequence 12, Appl
493	6	20.0	31	4	US-09-442-989-13	Sequence 13, Appl
494	6	20.0	31	4	US-09-442-989-14	Sequence 14, Appl
495	6	20.0	32	4	US-09-536-785A-37	Sequence 37, Appl
496	6	20.0	33	4	US-09-536-785A-38	Sequence 38, Appl
497	6	20.0	34	1	US-07-765-373-2	Sequence 2, Appli
498	6	20.0	34	1	US-08-049-402-1	Sequence 1, Appli
499	6	20.0	34	1	US-08-526-987-1	Sequence 1, Appli
500	6	20.0	34	4	US-09-536-785A-24	Sequence 24, Appl
501	6	20.0	35	4	US-09-536-785A-25	Sequence 25, Appl
502	6	20.0	36	4	US-09-536-785A-26	Sequence 26, Appl
503	6	20.0	37	4	US-09-536-785A-27	Sequence 27, Appl
504	5	16.7	29	1	US-08-188-582-33	Sequence 33, Appl
505	5	16.7	29	1	US-08-646-715-33	Sequence 33, Appl
506	5	16.7	30	1	US-08-305-799A-7	Sequence 7, Appli
507	5	16.7	30	1	US-08-305-799A-9	Sequence 9, Appli
508	5	16.7	30	1	US-08-305-799A-10	Sequence 10, Appl
509	5	16.7	30	1	US-08-305-799A-11	Sequence 11, Appl
510	5	16.7	30	1	US-08-305-799A-12	Sequence 12, Appl
511	5	16.7	34	1	US-08-449-500-37	Sequence 37, Appl
512	5	16.7	34	1	US-08-449-317A-37	Sequence 37, Appl
513	5	16.7	34	2	US-08-477-022-37	Sequence 37, Appl
514	5	16.7	34	2	US-08-449-447-37	Sequence 37, Appl
515	5	16.7	34	2	US-08-184-328-37	Sequence 37, Appl
516	5	16.7	34	2	US-08-521-097-37	Sequence 37, Appl
517	5	16.7	38	1	US-08-444-005-19	Sequence 19, Appl
518	4	13.3	28	1	US-07-899-535A-4	Sequence 4, Appli
519	4	13.3	28	1	US-08-191-866D-76	Sequence 76, Appl
520	4	13.3	28	2	US-08-185-949B-76	Sequence 76, Appl
521	4	13.3	28	2	US-08-620-151-126	Sequence 126, App
522	4	13.3	28	2	US-08-818-253-22	Sequence 22, Appl
523	4	13.3	28	3	US-08-641-873-8	Sequence 8, Appli
524	4	13.3	28	3	US-08-818-252-22	Sequence 22, Appl

525	4	13.3	28	4	US-08-842-322-16	Sequence 16, Appl
526	4	13.3	28	4	US-09-316-919-38	Sequence 38, Appl
527	4	13.3	28	4	US-09-323-867A-153	Sequence 153, App
528	4	13.3	28	5	PCT-US92-07813-3	Sequence 3, Appli
529	4	13.3	29	4	US-09-227-357-386	Sequence 386, App
530	4	13.3	29	4	US-09-227-357-480	Sequence 480, App
531	4	13.3	29	4	US-09-695-458-8	Sequence 8, Appli
532	4	13.3	29	4	US-09-205-258-1006	Sequence 1006, Ap
533	4	13.3	30	1	US-08-305-799A-3	Sequence 3, Appli
534	4	13.3	30	1	US-08-305-799A-4	Sequence 4, Appli
535	4	13.3	30	4	US-09-205-258-821	Sequence 821, App
536	4	13.3	31	1	US-07-829-462-3	Sequence 3, Appli
537	4	13.3	31	1	US-08-340-812-3	Sequence 3, Appli
538	4	13.3	31	1	US-08-248-021A-5	Sequence 5, Appli
539	4	13.3	31	1	US-08-323-531-44	Sequence 44, Appl
540	4	13.3	31	1	US-08-323-531-50	Sequence 50, Appl
541	4	13.3	31	1	US-08-323-531-62	Sequence 62, Appl
542	4	13.3	31	1	US-08-198-094-44	Sequence 44, Appl
543	4	13.3	31	1	US-08-198-094-50	Sequence 50, Appl
544	4	13.3	31	1	US-08-198-094-62	Sequence 62, Appl
545	4	13.3	31	1	US-08-459-064B-3	Sequence 3, Appli
546	4	13.3	31	2	US-08-460-421A-3	Sequence 3, Appli
547	4	13.3	31	2	US-08-663-566A-32	Sequence 32, Appl
548	4	13.3	31	2	US-08-023-610-32	Sequence 32, Appl
549	4	13.3	31	2	US-08-288-065A-32	Sequence 32, Appl
550	4	13.3	31	2	US-08-362-240A-32	Sequence 32, Appl
551	4	13.3	31	3	US-08-107-794A-44	Sequence 44, Appl
552	4	13.3	31	3	US-08-107-794A-50	Sequence 50, Appl
553	4	13.3	31	3	US-08-107-794A-62	Sequence 62, Appl
554	4	13.3	31	4	US-09-205-258-1001	Sequence 1001, Ap
555	4	13.3	31	5	PCT-US93-00909-3	Sequence 3, Appli
556	4	13.3	31	5	PCT-US93-07424-44	Sequence 44, Appl
557	4	13.3	31	5	PCT-US93-07424-50	Sequence 50, Appl
558	4	13.3	31	5	PCT-US93-07424-62	Sequence 62, Appl
559	4	13.3	31	5	PCT-US95-02087-44	Sequence 44, Appl
560	4	13.3	31	5	PCT-US95-02087-50	Sequence 50, Appl
561	4	13.3	31	5	PCT-US95-02087-62	Sequence 62, Appl
562	4	13.3	31	5	PCT-US95-10245-32	Sequence 32, Appl
563	4	13.3	32	1	US-08-190-802A-110	Sequence 110, App
564	4	13.3	32	1	US-08-190-802A-114	Sequence 114, App
565	4	13.3	32	1	US-08-190-802A-183	Sequence 183, App
566	4	13.3	32	1	US-08-190-802A-216	Sequence 216, App
567	4	13.3	32	3	US-08-477-346-110	Sequence 110, App
568	4	13.3	32	3	US-08-477-346-114	Sequence 114, App
569	4	13.3	32	3	US-08-477-346-183	Sequence 183, App
570	4	13.3	32	3	US-08-477-346-216	Sequence 216, App
571	4	13.3	32	4	US-08-473-089-110	Sequence 110, App
572	4	13.3	32	4	US-08-473-089-114	Sequence 114, App
573	4	13.3	32	4	US-08-473-089-183	Sequence 183, App
574	4	13.3	32	4	US-08-473-089-216	Sequence 216, App
575	4	13.3	32	4	US-09-149-476-442	Sequence 442, App
576	4	13.3	32	4	US-08-487-072A-110	Sequence 110, App
577	4	13.3	32	4	US-08-487-072A-114	Sequence 114, App
578	4	13.3	32	4	US-08-487-072A-183	Sequence 183, App
579	4	13.3	32	4	US-08-487-072A-216	Sequence 216, App
580	4	13.3	33	1	US-08-781-020-10	Sequence 10, Appl
581	4	13.3	33	3	US-09-038-935-10	Sequence 10, Appl

582	4	13.3	33	4	US-09-149-476-660	Sequence 660, App
583	4	13.3	33	4	US-09-122-144-4	Sequence 4, Appli
584	4	13.3	33	4	US-09-205-258-368	Sequence 368, App
585	4	13.3	34	1	US-08-007-775-1	Sequence 1, Appli
586	4	13.3	34	1	US-07-956-700B-7	Sequence 7, Appli
587	4	13.3	34	1	US-08-476-537-7	Sequence 7, Appli
588	4	13.3	34	1	US-08-485-607-7	Sequence 7, Appli
589	4	13.3	34	2	US-08-475-879-7	Sequence 7, Appli
590	4	13.3	34	4	US-09-433-043B-7	Sequence 7, Appli
591	4	13.3	35	1	US-08-463-660-6	Sequence 6, Appli
592	4	13.3	35	1	US-08-678-280-6	Sequence 6, Appli
593	4	13.3	35	4	US-09-227-357-486	Sequence 486, App
594	4	13.3	35	4	US-09-690-454-138	Sequence 138, App
595	4	13.3	36	1	US-08-477-727A-104	Sequence 104, App
596	4	13.3	36	1	US-08-471-675A-26	Sequence 26, Appl
597	4	13.3	36	2	US-08-892-549-30	Sequence 30, Appl
598	4	13.3	36	3	US-08-302-069A-25	Sequence 25, Appl
599	4	13.3	37	1	US-08-231-730A-45	Sequence 45, Appl
600	4	13.3	37	1	US-08-477-727A-102	Sequence 102, App
601	4	13.3	37	1	US-08-477-727A-103	Sequence 103, App
602	4	13.3	37	1	US-08-477-727A-105	Sequence 105, App
603	4	13.3	37	1	US-08-477-727A-106	Sequence 106, App
604	4	13.3	37	1	US-08-477-727A-107	Sequence 107, App
605	4	13.3	37	1	US-08-471-675A-24	Sequence 24, Appl
606	4	13.3	37	1	US-08-471-675A-25	Sequence 25, Appl
607	4	13.3	37	1	US-08-471-675A-27	Sequence 27, Appl
608	4	13.3	37	1	US-08-471-675A-28	Sequence 28, Appl
609	4	13.3	37	1	US-08-471-675A-29	Sequence 29, Appl
610	4	13.3	37	2	US-08-259-762-12	Sequence 12, Appl
611	4	13.3	37	2	US-08-259-762-13	Sequence 13, Appl
612	4	13.3	37	2	US-08-283-917-12	Sequence 12, Appl
613	4	13.3	37	2	US-08-961-716-12	Sequence 12, Appl
614	4	13.3	37	2	US-08-505-486-50	Sequence 50, Appl
615	4	13.3	37	2	US-08-892-549-6	Sequence 6, Appli
616	4	13.3	37	2	US-08-892-549-28	Sequence 28, Appl
617	4	13.3	37	2	US-08-892-549-29	Sequence 29, Appl
618	4	13.3	37	2	US-08-892-549-31	Sequence 31, Appl
619	4	13.3	37	2	US-08-892-549-32	Sequence 32, Appl
620	4	13.3	37	2	US-08-892-549-33	Sequence 33, Appl
621	4	13.3	37	3	US-08-689-489C-45	Sequence 45, Appl
622	4	13.3	37	3	US-08-801-028-50	Sequence 50, Appl
623	4	13.3	37	3	US-09-340-154-50	Sequence 50, Appl
624	4	13.3	37	3	US-08-302-069A-23	Sequence 23, Appl
625	4	13.3	37	3	US-08-302-069A-24	Sequence 24, Appl
626	4	13.3	37	3	US-08-302-069A-26	Sequence 26, Appl
627	4	13.3	37	3	US-08-302-069A-27	Sequence 27, Appl
628	4	13.3	37	3	US-08-302-069A-28	Sequence 28, Appl
629	4	13.3	37	3	US-09-232-802A-45	Sequence 45, Appl
630	4	13.3	37	4	US-09-482-611B-50	Sequence 50, Appl
631	4	13.3	37	5	PCT-US95-04718-45	Sequence 45, Appl
632	4	13.3	37	5	PCT-US95-09338-50	Sequence 50, Appl
633	4	13.3	37	5	PCT-US95-09339-50	Sequence 50, Appl
634	4	13.3	38	1	US-07-781-254A-18	Sequence 18, Appl
635	4	13.3	38	2	US-08-378-548-12	Sequence 12, Appl
636	4	13.3	39	4	US-09-227-357-384	Sequence 384, App
637	4	13.3	39	4	US-09-323-867A-25	Sequence 25, Appl
638	3	10.0	28	1	US-07-620-410-2	Sequence 2, Appli

639	3	10.0	28	1	US-07-690-300B-1	Sequence 1, Appli
640	3	10.0	28	1	US-07-690-300B-12	Sequence 12, Appl
641	3	10.0	28	1	US-07-690-300B-23	Sequence 23, Appl
642	3	10.0	28	1	US-07-690-300B-24	Sequence 24, Appl
643	3	10.0	28	1	US-07-690-300B-25	Sequence 25, Appl
644	3	10.0	28	1	US-07-690-300B-26	Sequence 26, Appl
645	3	10.0	28	1	US-07-690-300B-27	Sequence 27, Appl
646	3	10.0	28	1	US-07-690-300B-28	Sequence 28, Appl
647	3	10.0	28	1	US-07-690-300B-29	Sequence 29, Appl
648	3	10.0	28	1	US-07-690-300B-30	Sequence 30, Appl
649	3	10.0	28	1	US-07-690-300B-31	Sequence 31, Appl
650	3	10.0	28	1	US-07-690-300B-32	Sequence 32, Appl
651	3	10.0	28	1	US-07-690-300B-33	Sequence 33, Appl
652	3	10.0	28	1	US-07-690-300B-34	Sequence 34, Appl
653	3	10.0	28	1	US-07-690-300B-35	Sequence 35, Appl
654	3	10.0	28	1	US-07-690-300B-36	Sequence 36, Appl
655	3	10.0	28	1	US-07-690-300B-37	Sequence 37, Appl
656	3	10.0	28	1	US-07-690-300B-38	Sequence 38, Appl
657	3	10.0	28	1	US-07-690-300B-39	Sequence 39, Appl
658	3	10.0	28	1	US-07-690-300B-40	Sequence 40, Appl
659	3	10.0	28	1	US-07-690-300B-41	Sequence 41, Appl
660	3	10.0	28	1	US-07-690-300B-42	Sequence 42, Appl
661	3	10.0	28	1	US-07-690-300B-43	Sequence 43, Appl
662	3	10.0	28	1	US-07-690-300B-44	Sequence 44, Appl
663	3	10.0	28	1	US-07-690-300B-45	Sequence 45, Appl
664	3	10.0	28	1	US-07-690-300B-46	Sequence 46, Appl
665	3	10.0	28	1	US-07-690-300B-47	Sequence 47, Appl
666	3	10.0	28	1	US-07-690-300B-48	Sequence 48, Appl
667	3	10.0	28	1	US-07-690-300B-49	Sequence 49, Appl
668	3	10.0	28	1	US-07-690-300B-50	Sequence 50, Appl
669	3	10.0	28	1	US-07-690-300B-51	Sequence 51, Appl
670	3	10.0	28	1	US-07-690-300B-52	Sequence 52, Appl
671	3	10.0	28	1	US-07-690-300B-53	Sequence 53, Appl
672	3	10.0	28	1	US-07-690-300B-54	Sequence 54, Appl
673	3	10.0	28	1	US-07-690-300B-55	Sequence 55, Appl
674	3	10.0	28	1	US-07-690-300B-56	Sequence 56, Appl
675	3	10.0	28	1	US-07-690-300B-63	Sequence 63, Appl
676	3	10.0	28	1	US-07-690-300B-64	Sequence 64, Appl
677	3	10.0	28	1	US-07-690-300B-68	Sequence 68, Appl
678	3	10.0	28	1	US-07-690-300B-71	Sequence 71, Appl
679	3	10.0	28	1	US-07-690-300B-78	Sequence 78, Appl
680	3	10.0	28	1	US-07-690-300B-79	Sequence 79, Appl
681	3	10.0	28	1	US-07-690-300B-82	Sequence 82, Appl
682	3	10.0	28	1	US-07-690-300B-88	Sequence 88, Appl
683	3	10.0	28	1	US-07-690-300B-91	Sequence 91, Appl
684	3	10.0	28	1	US-07-690-300B-93	Sequence 93, Appl
685	3	10.0	28	1	US-07-663-413-29	Sequence 29, Appl
686	3	10.0	28	1	US-07-676-987A-1	Sequence 1, Appli
687	3	10.0	28	1	US-07-676-987A-2	Sequence 2, Appli
688	3	10.0	28	1	US-07-833-468-1	Sequence 1, Appli
689	3	10.0	28	1	US-08-052-681-10	Sequence 10, Appl
690	3	10.0	28	1	US-07-789-344A-11	Sequence 11, Appl
691	3	10.0	28	1	US-07-868-906-1	Sequence 1, Appli
692	3	10.0	28	1	US-08-201-092-1	Sequence 1, Appli
693	3	10.0	28	1	US-08-201-092-2	Sequence 2, Appli
694	3	10.0	28	1	US-08-055-530-29	Sequence 29, Appl
695	3	10.0	28	1	US-08-122-578-1	Sequence 1, Appli

696	3	10.0	28	1	US-08-032-848C-1	Sequence 1, Appli
697	3	10.0	28	1	US-07-966-187-2	Sequence 2, Appli
698	3	10.0	28	1	US-08-255-558B-6	Sequence 6, Appli
699	3	10.0	28	1	US-07-924-054-11	Sequence 11, Appl
700	3	10.0	28	1	US-08-243-082-1	Sequence 1, Appli
701	3	10.0	28	1	US-08-246-572-4	Sequence 4, Appli
702	3	10.0	28	1	US-08-246-572-5	Sequence 5, Appli
703	3	10.0	28	1	US-08-190-802A-84	Sequence 84, Appl
704	3	10.0	28	1	US-08-361-443-1	Sequence 1, Appli
705	3	10.0	28	1	US-08-311-611A-12	Sequence 12, Appl
706	3	10.0	28	1	US-08-311-611A-56	Sequence 56, Appl
707	3	10.0	28	1	US-08-311-611A-193	Sequence 193, App
708	3	10.0	28	1	US-08-311-611A-194	Sequence 194, App
709	3	10.0	28	1	US-08-311-611A-195	Sequence 195, App
710	3	10.0	28	1	US-08-311-611A-196	Sequence 196, App
711	3	10.0	28	1	US-07-938-782A-8	Sequence 8, Appli
712	3	10.0	28	1	US-07-949-797B-1	Sequence 1, Appli
713	3	10.0	28	1	US-08-194-591-1	Sequence 1, Appli
714	3	10.0	28	1	US-08-194-591-2	Sequence 2, Appli
715	3	10.0	28	1	US-08-257-446-6	Sequence 6, Appli
716	3	10.0	28	1	US-08-372-783-12	Sequence 12, Appl
717	3	10.0	28	1	US-08-372-783-56	Sequence 56, Appl
718	3	10.0	28	1	US-08-372-783-193	Sequence 193, App
719	3	10.0	28	1	US-08-372-783-194	Sequence 194, App
720	3	10.0	28	1	US-08-372-783-195	Sequence 195, App
721	3	10.0	28	1	US-08-372-783-196	Sequence 196, App
722	3	10.0	28	1	US-07-794-288D-7	Sequence 7, Appli
723	3	10.0	28	1	US-07-794-288D-65	Sequence 65, Appl
724	3	10.0	28	1	US-07-794-288D-103	Sequence 103, App
725	3	10.0	28	1	US-07-977-630-42	Sequence 42, Appl
726	3	10.0	28	1	US-07-977-630-45	Sequence 45, Appl
727	3	10.0	28	1	US-07-977-630-47	Sequence 47, Appl
728	3	10.0	28	1	US-08-288-681A-1	Sequence 1, Appli
729	3	10.0	28	1	US-08-366-591-12	Sequence 12, Appl
730	3	10.0	28	1	US-07-776-272-26	Sequence 26, Appl
731	3	10.0	28	1	US-08-372-105-12	Sequence 12, Appl
732	3	10.0	28	1	US-08-372-105-56	Sequence 56, Appl
733	3	10.0	28	1	US-08-372-105-193	Sequence 193, App
734	3	10.0	28	1	US-08-372-105-194	Sequence 194, App
735	3	10.0	28	1	US-08-372-105-195	Sequence 195, App
736	3	10.0	28	1	US-08-372-105-196	Sequence 196, App
737	3	10.0	28	1	US-08-306-473A-12	Sequence 12, Appl
738	3	10.0	28	1	US-08-306-473A-56	Sequence 56, Appl
739	3	10.0	28	1	US-08-306-473A-193	Sequence 193, App
740	3	10.0	28	1	US-08-306-473A-194	Sequence 194, App
741	3	10.0	28	1	US-08-306-473A-195	Sequence 195, App
742	3	10.0	28	1	US-08-306-473A-196	Sequence 196, App
743	3	10.0	28	1	US-08-331-394-19	Sequence 19, Appl
744	3	10.0	28	1	US-08-308-729-1	Sequence 1, Appli
745	3	10.0	28	1	US-08-308-729-2	Sequence 2, Appli
746	3	10.0	28	1	US-08-308-729-3	Sequence 3, Appli
747	3	10.0	28	1	US-08-308-729-4	Sequence 4, Appli
748	3	10.0	28	1	US-08-308-729-5	Sequence 5, Appli
749	3	10.0	28	1	US-08-308-729-6	Sequence 6, Appli
750	3	10.0	28	1	US-08-308-729-7	Sequence 7, Appli
751	3	10.0	28	1	US-08-308-729-8	Sequence 8, Appli
752	3	10.0	28	1	US-08-308-729-9	Sequence 9, Appli

753	3	10.0	28	1	US-08-308-729-10	Sequence 10, Appl
754	3	10.0	28	1	US-08-308-729-11	Sequence 11, Appl
755	3	10.0	28	1	US-08-308-729-12	Sequence 12, Appl
756	3	10.0	28	1	US-08-308-729-13	Sequence 13, Appl
757	3	10.0	28	1	US-08-308-729-14	Sequence 14, Appl
758	3	10.0	28	1	US-08-308-729-15	Sequence 15, Appl
759	3	10.0	28	1	US-08-308-729-16	Sequence 16, Appl
760	3	10.0	28	1	US-08-308-729-17	Sequence 17, Appl
761	3	10.0	28	1	US-08-308-729-18	Sequence 18, Appl
762	3	10.0	28	1	US-08-308-729-19	Sequence 19, Appl
763	3	10.0	28	1	US-08-308-729-20	Sequence 20, Appl
764	3	10.0	28	1	US-08-308-729-21	Sequence 21, Appl
765	3	10.0	28	1	US-08-308-729-22	Sequence 22, Appl
766	3	10.0	28	1	US-08-308-729-23	Sequence 23, Appl
767	3	10.0	28	1	US-08-308-729-24	Sequence 24, Appl
768	3	10.0	28	1	US-08-308-729-25	Sequence 25, Appl
769	3	10.0	28	1	US-08-308-729-26	Sequence 26, Appl
770	3	10.0	28	1	US-08-308-729-27	Sequence 27, Appl
771	3	10.0	28	1	US-08-308-729-28	Sequence 28, Appl
772	3	10.0	28	1	US-08-308-729-29	Sequence 29, Appl
773	3	10.0	28	1	US-08-308-729-31	Sequence 31, Appl
774	3	10.0	28	1	US-08-308-729-33	Sequence 33, Appl
775	3	10.0	28	1	US-08-308-729-34	Sequence 34, Appl
776	3	10.0	28	1	US-08-308-729-35	Sequence 35, Appl
777	3	10.0	28	1	US-08-308-729-36	Sequence 36, Appl
778	3	10.0	28	1	US-08-308-729-37	Sequence 37, Appl
779	3	10.0	28	1	US-08-308-729-38	Sequence 38, Appl
780	3	10.0	28	1	US-08-308-729-39	Sequence 39, Appl
781	3	10.0	28	1	US-08-308-729-40	Sequence 40, Appl
782	3	10.0	28	1	US-08-308-729-41	Sequence 41, Appl
783	3	10.0	28	1	US-08-308-729-44	Sequence 44, Appl
784	3	10.0	28	1	US-08-308-729-45	Sequence 45, Appl
785	3	10.0	28	1	US-08-308-729-46	Sequence 46, Appl
786	3	10.0	28	1	US-08-308-729-47	Sequence 47, Appl
787	3	10.0	28	1	US-08-308-729-48	Sequence 48, Appl
788	3	10.0	28	1	US-08-308-729-49	Sequence 49, Appl
789	3	10.0	28	1	US-08-308-729-50	Sequence 50, Appl
790	3	10.0	28	1	US-08-308-729-53	Sequence 53, Appl
791	3	10.0	28	1	US-08-308-729-54	Sequence 54, Appl
792	3	10.0	28	1	US-08-308-729-55	Sequence 55, Appl
793	3	10.0	28	1	US-08-308-729-56	Sequence 56, Appl
794	3	10.0	28	1	US-08-308-729-57	Sequence 57, Appl
795	3	10.0	28	1	US-08-308-729-58	Sequence 58, Appl
796	3	10.0	28	1	US-08-308-729-59	Sequence 59, Appl
797	3	10.0	28	1	US-08-308-729-60	Sequence 60, Appl
798	3	10.0	28	1	US-08-308-729-61	Sequence 61, Appl
799	3	10.0	28	1	US-08-308-729-62	Sequence 62, Appl
800	3	10.0	28	1	US-08-308-729-63	Sequence 63, Appl
801	3	10.0	28	1	US-08-308-729-64	Sequence 64, Appl
802	3	10.0	28	1	US-08-308-729-70	Sequence 70, Appl
803	3	10.0	28	1	US-08-308-729-71	Sequence 71, Appl
804	3	10.0	28	1	US-08-308-729-72	Sequence 72, Appl
805	3	10.0	28	1	US-08-308-729-73	Sequence 73, Appl
806	3	10.0	28	1	US-08-630-524-8	Sequence 8, Appli
807	3	10.0	28	1	US-08-062-472B-40	Sequence 40, Appl
808	3	10.0	28	1	US-08-250-858-19	Sequence 19, Appl
809	3	10.0	28	1	US-08-171-701A-1	Sequence 1, Appli

810	3	10.0	28	1	US-08-171-701A-2	Sequence 2, Appli
811	3	10.0	28	1	US-08-261-660A-19	Sequence 19, Appl
812	3	10.0	28	1	US-08-741-678-1	Sequence 1, Appli
813	3	10.0	28	1	US-08-209-762-12	Sequence 12, Appl
814	3	10.0	28	1	US-08-209-762-56	Sequence 56, Appl
815	3	10.0	28	1	US-08-446-915-19	Sequence 19, Appl
816	3	10.0	28	1	US-08-404-731A-8	Sequence 8, Appli
817	3	10.0	28	1	US-08-438-870-1	Sequence 1, Appli
818	3	10.0	28	1	US-08-442-029-9	Sequence 9, Appli
819	3	10.0	28	1	US-08-446-692-3	Sequence 3, Appli
820	3	10.0	28	1	US-08-473-344-12	Sequence 12, Appl
821	3	10.0	28	1	US-08-473-344-56	Sequence 56, Appl
822	3	10.0	28	1	US-08-519-180-2	Sequence 2, Appli
823	3	10.0	28	1	US-08-944-133-4	Sequence 4, Appli
824	3	10.0	28	1	US-08-944-133-8	Sequence 8, Appli
825	3	10.0	28	1	US-08-944-133-22	Sequence 22, Appl
826	3	10.0	28	1	US-08-944-133-27	Sequence 27, Appl
827	3	10.0	28	1	US-08-944-133-39	Sequence 39, Appl
828	3	10.0	28	1	US-08-944-133-43	Sequence 43, Appl
829	3	10.0	28	2	US-08-520-535-25	Sequence 25, Appl
830	3	10.0	28	2	US-08-488-351A-3	Sequence 3, Appli
831	3	10.0	28	2	US-08-414-424-1	Sequence 1, Appli
832	3	10.0	28	2	US-08-621-803-30	Sequence 30, Appl
833	3	10.0	28	2	US-08-621-803-139	Sequence 139, App
834	3	10.0	28	2	US-08-621-803-140	Sequence 140, App
835	3	10.0	28	2	US-08-621-803-142	Sequence 142, App
836	3	10.0	28	2	US-08-621-803-143	Sequence 143, App
837	3	10.0	28	2	US-08-485-445A-12	Sequence 12, Appl
838	3	10.0	28	2	US-08-485-445A-56	Sequence 56, Appl
839	3	10.0	28	2	US-08-485-445A-193	Sequence 193, App
840	3	10.0	28	2	US-08-485-445A-194	Sequence 194, App
841	3	10.0	28	2	US-08-485-445A-195	Sequence 195, App
842	3	10.0	28	2	US-08-485-445A-196	Sequence 196, App
843	3	10.0	28	2	US-08-621-259A-5	Sequence 5, Appli
844	3	10.0	28	2	US-08-621-259A-110	Sequence 110, App
845	3	10.0	28	2	US-08-621-259A-111	Sequence 111, App
846	3	10.0	28	2	US-08-621-259A-113	Sequence 113, App
847	3	10.0	28	2	US-08-621-259A-114	Sequence 114, App
848	3	10.0	28	2	US-08-449-933-9	Sequence 9, Appli
849	3	10.0	28	2	US-08-744-139-19	Sequence 19, Appl
850	3	10.0	28	2	US-08-503-226B-8	Sequence 8, Appli
851	3	10.0	28	2	US-08-598-873-43	Sequence 43, Appl
852	3	10.0	28	2	US-08-620-151-66	Sequence 66, Appl
853	3	10.0	28	2	US-08-620-151-129	Sequence 129, App
854	3	10.0	28	2	US-08-398-590A-43	Sequence 43, Appl
855	3	10.0	28	2	US-08-821-619-10	Sequence 10, Appl
856	3	10.0	28	2	US-08-635-007-8	Sequence 8, Appli
857	3	10.0	28	2	US-09-079-432-25	Sequence 25, Appl
858	3	10.0	28	2	US-08-859-106A-8	Sequence 8, Appli
859	3	10.0	28	2	US-08-833-377-11	Sequence 11, Appl
860	3	10.0	28	2	US-08-031-538-48	Sequence 48, Appl
861	3	10.0	28	2	US-08-413-708B-1	Sequence 1, Appli
862	3	10.0	28	2	US-08-413-708B-2	Sequence 2, Appli
863	3	10.0	28	2	US-08-413-708B-8	Sequence 8, Appli
864	3	10.0	28	2	US-08-563-892A-4	Sequence 4, Appli
865	3	10.0	28	2	US-08-691-814B-73	Sequence 73, Appl
866	3	10.0	28	2	US-08-818-253-37	Sequence 37, Appl

867	3	10.0	28	2	US-08-897-624-1	Sequence 1, Appli
868	3	10.0	28	2	US-08-897-624-2	Sequence 2, Appli
869	3	10.0	28	3	US-09-110-953-8	Sequence 8, Appli
870	3	10.0	28	3	US-08-930-845-1	Sequence 1, Appli
871	3	10.0	28	3	US-08-486-099-84	Sequence 84, Appl
872	3	10.0	28	3	US-08-486-099-136	Sequence 136, App
873	3	10.0	28	3	US-08-433-522A-34	Sequence 34, Appl
874	3	10.0	28	3	US-08-360-107A-94	Sequence 94, Appl
875	3	10.0	28	3	US-08-788-231A-18	Sequence 18, Appl
876	3	10.0	28	3	US-08-484-223B-84	Sequence 84, Appl
877	3	10.0	28	3	US-08-484-223B-136	Sequence 136, App
878	3	10.0	28	3	US-09-100-414B-38	Sequence 38, Appl
879	3	10.0	28	3	US-08-665-259-18	Sequence 18, Appl
880	3	10.0	28	3	US-08-762-500-18	Sequence 18, Appl
881	3	10.0	28	3	US-08-952-568-1	Sequence 1, Appli
882	3	10.0	28	3	US-08-952-568-3	Sequence 3, Appli
883	3	10.0	28	3	US-08-952-568-4	Sequence 4, Appli
884	3	10.0	28	3	US-08-952-568-5	Sequence 5, Appli
885	3	10.0	28	3	US-08-952-568-6	Sequence 6, Appli
886	3	10.0	28	3	US-08-952-568-10	Sequence 10, Appl
887	3	10.0	28	3	US-08-952-568-11	Sequence 11, Appl
888	3	10.0	28	3	US-08-952-568-12	Sequence 12, Appl
889	3	10.0	28	3	US-08-952-568-13	Sequence 13, Appl
890	3	10.0	28	3	US-08-952-568-14	Sequence 14, Appl
891	3	10.0	28	3	US-08-256-747C-50	Sequence 50, Appl
892	3	10.0	28	3	US-08-919-597-84	Sequence 84, Appl
893	3	10.0	28	3	US-08-919-597-136	Sequence 136, App
894	3	10.0	28	3	US-09-119-263-12	Sequence 12, Appl
895	3	10.0	28	3	US-09-119-263-56	Sequence 56, Appl
896	3	10.0	28	3	US-09-119-263-193	Sequence 193, App
897	3	10.0	28	3	US-09-119-263-194	Sequence 194, App
898	3	10.0	28	3	US-09-119-263-195	Sequence 195, App
899	3	10.0	28	3	US-09-119-263-196	Sequence 196, App
900	3	10.0	28	3	US-08-475-668A-84	Sequence 84, Appl
901	3	10.0	28	3	US-08-475-668A-136	Sequence 136, App
902	3	10.0	28	3	US-09-192-048-21	Sequence 21, Appl
903	3	10.0	28	3	US-08-485-551A-84	Sequence 84, Appl
904	3	10.0	28	3	US-08-485-551A-136	Sequence 136, App
905	3	10.0	28	3	US-08-838-413A-6	Sequence 6, Appli
906	3	10.0	28	3	US-09-135-166-34	Sequence 34, Appl
907	3	10.0	28	3	US-08-471-913A-84	Sequence 84, Appl
908	3	10.0	28	3	US-08-471-913A-136	Sequence 136, App
909	3	10.0	28	3	US-08-721-458B-8	Sequence 8, Appli
910	3	10.0	28	3	US-08-908-643C-43	Sequence 43, Appl
911	3	10.0	28	3	US-08-405-647B-39	Sequence 39, Appl
912	3	10.0	28	3	US-08-893-749-2	Sequence 2, Appli
913	3	10.0	28	3	US-08-893-749-3	Sequence 3, Appli
914	3	10.0	28	3	US-08-893-749-32	Sequence 32, Appl
915	3	10.0	28	3	US-08-657-162-12	Sequence 12, Appl
916	3	10.0	28	3	US-08-657-162-56	Sequence 56, Appl
917	3	10.0	28	3	US-08-657-162-193	Sequence 193, App
918	3	10.0	28	3	US-08-657-162-194	Sequence 194, App
919	3	10.0	28	3	US-08-657-162-195	Sequence 195, App
920	3	10.0	28	3	US-08-657-162-196	Sequence 196, App
921	3	10.0	28	3	US-09-433-428D-62	Sequence 62, Appl
922	3	10.0	28	3	US-08-679-006-15	Sequence 15, Appl
923	3	10.0	28	3	US-09-224-480-12	Sequence 12, Appl

924	3	10.0	28	3	US-09-224-480-56	Sequence 56, Appl
925	3	10.0	28	3	US-09-224-480-193	Sequence 193, App
926	3	10.0	28	3	US-09-224-480-194	Sequence 194, App
927	3	10.0	28	3	US-09-224-480-195	Sequence 195, App
928	3	10.0	28	3	US-09-224-480-196	Sequence 196, App
929	3	10.0	28	3	US-08-796-899-30	Sequence 30, Appl
930	3	10.0	28	3	US-08-974-549A-166	Sequence 166, App
931	3	10.0	28	3	US-08-392-542-22	Sequence 22, Appl
932	3	10.0	28	3	US-08-819-286-29	Sequence 29, Appl
933	3	10.0	28	3	US-08-817-811-13	Sequence 13, Appl
934	3	10.0	28	3	US-08-817-811-14	Sequence 14, Appl
935	3	10.0	28	3	US-08-817-811-15	Sequence 15, Appl
936	3	10.0	28	3	US-08-817-811-66	Sequence 66, Appl
937	3	10.0	28	3	US-08-817-811-67	Sequence 67, Appl
938	3	10.0	28	3	US-08-834-130A-50	Sequence 50, Appl
939	3	10.0	28	3	US-08-448-398-12	Sequence 12, Appl
940	3	10.0	28	3	US-09-058-459-19	Sequence 19, Appl
941	3	10.0	28	3	US-08-985-499-39	Sequence 39, Appl
942	3	10.0	28	3	US-08-818-252-37	Sequence 37, Appl
943	3	10.0	28	3	US-08-363-558-1	Sequence 1, Appli
944	3	10.0	28	3	US-09-066-046-19	Sequence 19, Appl
945	3	10.0	28	3	US-09-253-396A-223	Sequence 223, App
946	3	10.0	28	3	US-09-107-991-12	Sequence 12, Appl
947	3	10.0	28	3	US-09-093-539-12	Sequence 12, Appl
948	3	10.0	28	3	US-09-093-539-56	Sequence 56, Appl
949	3	10.0	28	3	US-08-485-264A-84	Sequence 84, Appl
950	3	10.0	28	3	US-08-485-264A-136	Sequence 136, App
951	3	10.0	28	3	US-09-303-323-38	Sequence 38, Appl
952	3	10.0	28	3	US-09-041-886-36	Sequence 36, Appl
953	3	10.0	28	3	US-09-041-886-37	Sequence 37, Appl
954	3	10.0	28	3	US-09-041-886-38	Sequence 38, Appl
955	3	10.0	28	3	US-09-041-886-39	Sequence 39, Appl
956	3	10.0	28	3	US-09-041-886-40	Sequence 40, Appl
957	3	10.0	28	3	US-09-041-886-42	Sequence 42, Appl
958	3	10.0	28	3	US-09-041-886-47	Sequence 47, Appl
959	3	10.0	28	3	US-09-041-886-50	Sequence 50, Appl
960	3	10.0	28	3	US-09-041-886-53	Sequence 53, Appl
961	3	10.0	28	3	US-09-041-886-54	Sequence 54, Appl
962	3	10.0	28	3	US-09-041-886-56	Sequence 56, Appl
963	3	10.0	28	3	US-09-127-680-2	Sequence 2, Appli
964	3	10.0	28	3	US-07-966-049A-9	Sequence 9, Appli
965	3	10.0	28	3	US-08-995-369-1	Sequence 1, Appli
966	3	10.0	28	3	US-09-171-654-1	Sequence 1, Appli
967	3	10.0	28	3	US-08-605-430-43	Sequence 43, Appl
968	3	10.0	28	3	US-08-894-327-22	Sequence 22, Appl
969	3	10.0	28	3	US-09-082-279B-54	Sequence 54, Appl
970	3	10.0	28	3	US-09-082-279B-62	Sequence 62, Appl
971	3	10.0	28	3	US-09-082-279B-1279	Sequence 1279, Ap
972	3	10.0	28	3	US-09-082-279B-1280	Sequence 1280, Ap
973	3	10.0	28	3	US-09-082-279B-1314	Sequence 1314, Ap
974	3	10.0	28	3	US-09-082-279B-1315	Sequence 1315, Ap
975	3	10.0	28	3	US-08-477-346-84	Sequence 84, Appl
976	3	10.0	28	3	US-08-942-046-34	Sequence 34, Appl
977	3	10.0	28	3	US-09-127-926-19	Sequence 19, Appl
978	3	10.0	28	3	US-08-894-997-43	Sequence 43, Appl
979	3	10.0	28	3	US-09-217-352-30	Sequence 30, Appl
980	3	10.0	28	3	US-09-217-352-139	Sequence 139, App

981	3	10.0	28	3	US-09-217-352-140	Sequence 140, App
982	3	10.0	28	3	US-09-217-352-142	Sequence 142, App
983	3	10.0	28	3	US-09-217-352-143	Sequence 143, App
984	3	10.0	28	3	US-09-019-095A-34	Sequence 34, Appl
985	3	10.0	28	4	US-09-260-846-16	Sequence 16, Appl
986	3	10.0	28	4	US-08-474-349A-84	Sequence 84, Appl
987	3	10.0	28	4	US-08-474-349A-136	Sequence 136, App
988	3	10.0	28	4	US-09-099-041A-19	Sequence 19, Appl
989	3	10.0	28	4	US-09-099-041A-23	Sequence 23, Appl
990	3	10.0	28	4	US-09-187-789-23	Sequence 23, Appl
991	3	10.0	28	4	US-08-473-089-84	Sequence 84, Appl
992	3	10.0	28	4	US-09-227-357-481	Sequence 481, App
993	3	10.0	28	4	US-09-227-357-531	Sequence 531, App
994	3	10.0	28	4	US-09-315-304B-54	Sequence 54, Appl
995	3	10.0	28	4	US-09-315-304B-62	Sequence 62, Appl
996	3	10.0	28	4	US-09-315-304B-1279	Sequence 1279, Ap
997	3	10.0	28	4	US-09-315-304B-1280	Sequence 1280, Ap
998	3	10.0	28	4	US-09-315-304B-1314	Sequence 1314, Ap
999	3	10.0	28	4	US-09-315-304B-1315	Sequence 1315, Ap
1000	3	10.0	28	4	US-09-432-879-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-08-262-495C-5

; Sequence 5, Application US/08262495C

; Patent No. 5556940

; GENERAL INFORMATION:

; APPLICANT: WILICK, Gordon E.

; APPLICANT: WHITFIELD, James F.

; APPLICANT: SUREWICZ, Witold

; APPLICANT: SUNG, Wing L.

; APPLICANT: NEUGENBAUER, Witold

; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kirby, Eades, Gale, Baker

; STREET: 112 Kent Street, Suite 770,

; CITY: Ottawa

; COUNTRY: Canada

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/262,495C

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-262-495C-5

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 2

US-08-262-495C-3

; Sequence 3, Application US/08262495C
; Patent No. 5556940
; GENERAL INFORMATION:
; APPLICANT: WILLICK, Gordon E.
; APPLICANT: WHITFIELD, James F.
; APPLICANT: SUREWICZ, Witold
; APPLICANT: SUNG, Wing L.
; APPLICANT: NEUGENBAUER, Witold
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kirby, Eades, Gale, Baker
; STREET: 112 Kent Street, Suite 770,
; CITY: Ottawa
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263

; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-262-495C-3

Query Match 100.0%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 3

US-08-691-647C-1

; Sequence 1, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene

; APPLICANT: Morley, Paul

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.

; STREET: 1100 New York Avenue, 8th Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/691,647C

; FILING DATE: August 2, 1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4005

; TELEFAX: (703) 816-4100
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-647C-1

Query Match 100.0%; Score 30; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 4

US-08-691-647C-6

; Sequence 6, Application US/08691647C
; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.
; STREET: 1100 New York Avenue, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/691,647C
; FILING DATE: August 2, 1996
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4005
; TELEFAX: (703) 816-4100
; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: cyclic
; MOLECULE TYPE: protein
US-08-691-647C-6

Query Match 100.0%; Score 30; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 5

US-08-904-760B-1

; Sequence 1, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:


```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 31 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: circular
;   MOLECULE TYPE: protein
;   FEATURE:
;   OTHER INFORMATION: cyclo Lys27-Asp30, and this sequence
;   OTHER INFORMATION: has an amino group c-terminus (NH2).
US-08-904-760B-6

```

```

Query Match          100.0%;  Score 30;  DB 3;  Length 31;
Best Local Similarity 100.0%;  Pred. No. 3.1e-22;
Matches 30;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 7

US-08-904-760B-14

```

; Sequence 14, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
;   APPLICANT: Jean-Rene, Barbier
;   APPLICANT: Neugebauer, Witold
;   APPLICANT: Ross, Virginia
;   APPLICANT: Whitfield, James
;   APPLICANT: Willick, Gordon E.
;   TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
;   TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: NIXON & VANDERHYE P.C.
;   STREET: 1100 No. 6110892th Glebe Rd. 8th floor
;   CITY: Arlington
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22201-4741
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/904,760B
;   FILING DATE: 01-AUG-1997
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/691,647
;   FILING DATE: 02-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Crawford, Arthur R.
;   REGISTRATION NUMBER: 25,327
;   REFERENCE/DOCKET NUMBER: 1339-6
;   TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; OTHER INFORMATION: cyclo Glu22-Lys26, and this sequence
 ; OTHER INFORMATION: has an amino group c-terminus (NH2).
 US-08-904-760B-14

Query Match 100.0%; Score 30; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e-22;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 8

US-08-904-760B-32

; Sequence 32, Application US/08904760B
 ; Patent No. 6110892
 ; GENERAL INFORMATION:
 ; APPLICANT: Jean-Rene, Barbier
 ; APPLICANT: Neugebauer, Witold
 ; APPLICANT: Ross, Virginia
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
 ; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201-4741
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/904,760B
 ; FILING DATE: 01-AUG-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/691,647
 ; FILING DATE: 02-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crawford, Arthur R.

```

;     REGISTRATION NUMBER: 25,327
;     REFERENCE/DOCKET NUMBER: 1339-6
;     TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-816-4000
;     TELEFAX: 703-816-4100
;     INFORMATION FOR SEQ ID NO: 32:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 31 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     FEATURE:
;     OTHER INFORMATION: This sequence has an amino group
;     OTHER INFORMATION: c-terminus (NH2).
US-08-904-760B-32

```

```

Query Match          100.0%;  Score 30;  DB 3;  Length 31;
Best Local Similarity 100.0%;  Pred. No. 3.1e-22;
Matches    30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 9

```

US-09-406-813-2
; Sequence 2, Application US/09406813
; Patent No. 6316410
; GENERAL INFORMATION:
; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 10688-1B
; CURRENT APPLICATION NUMBER: US/09/406,813
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: This sequence has an amino group c-terminus (NH2).
US-09-406-813-2

```

```

Query Match          100.0%;  Score 30;  DB 4;  Length 31;
Best Local Similarity 100.0%;  Pred. No. 3.1e-22;
Matches    30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```


Db |||||
1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 10

US-09-536-785A-1

; Sequence 1, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILLICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-536-785A-1

Query Match 100.0%; Score 30; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 11

US-09-536-785A-6

; Sequence 6, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILLICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF

```

; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)..(30)
; OTHER INFORMATION: Cyclo Lys27-Asp30
; OTHER INFORMATION: Amino c-terminus
US-09-536-785A-6

```

```

Query Match          100.0%; Score 30; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 12

```

US-09-536-785A-14
; Sequence 14, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560

```

; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (22)..(26)
; OTHER INFORMATION: Cyclo Glu22-Lys26
; OTHER INFORMATION: Amino c-terminus
US-09-536-785A-14

Query Match 100.0%; Score 30; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 13

US-09-536-785A-32
; Sequence 32, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino c-terminus
US-09-536-785A-32

Query Match 100.0%; Score 30; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.1e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 14

US-09-447-800-9

; Sequence 9, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-09-447-800-9

Query Match 100.0%; Score 30; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.3e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 15

US-07-765-373-1

; Sequence 1, Application US/07765373
; Patent No. 5393869
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: KAWASE, Masahiro
; APPLICANT: YAMAZAKI, Iwao
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/765,373
; FILING DATE: 19910925
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 41289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 20091 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-07-765-373-1

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 16

US-08-033-099-1

```

; Sequence 1, Application US/08033099
; Patent No. 5434246
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston

```

```

; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/033,099
; FILING DATE: 19930316
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 42528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (613)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-033-099-1

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 17

US-08-262-495C-1

```

; Sequence 1, Application US/08262495C
; Patent No. 5556940
; GENERAL INFORMATION:
; APPLICANT: WILLICK, Gordon E.
; APPLICANT: WHITFIELD, James F.
; APPLICANT: SUREWICZ, Witold
; APPLICANT: SUNG, Wing L.
; APPLICANT: NEUGENBAUER, Witold
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kirby, Eades, Gale, Baker
; STREET: 112 Kent Street, Suite 770,
; CITY: Ottawa
; COUNTRY: Canada
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-495C-1

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 18

US-07-915-247A-1

```

; Sequence 1, Application US/07915247A
; Patent No. 5589452
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,247A
; FILING DATE: 19920714
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-07-915-247A-1

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 19

US-08-443-863-1

```

; Sequence 1, Application US/08443863
; Patent No. 5693616

```

GENERAL INFORMATION:

```

; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:

```



```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,863
; FILING DATE: 14-JUL-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-443-863-1

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 20

```

US-08-448-070-1
; Sequence 1, Application US/08448070
; Patent No. 5695955
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,070
;      FILING DATE:  14-JUL-1992
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Schmonsees, William
;      REGISTRATION NUMBER:  31,796
;      REFERENCE/DOCKET NUMBER:  27610
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-6593
;      TELEFAX:  415-496-3529
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
;      HYPOTHETICAL:  NO
;      FRAGMENT TYPE:  N-terminal
US-08-448-070-1

```

```

Query Match          100.0%;  Score 30;  DB 1;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 3.4e-22;
Matches  30;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 21

```

US-08-488-105-7
; Sequence 7, Application US/08488105
; Patent No. 5717062
; GENERAL INFORMATION:
; APPLICANT:  Chorev, Michael
; APPLICANT:  Rosenblatt, Michael
; TITLE OF INVENTION:  CYCLIC ANALOGS OF PTH AND PTHrP
; NUMBER OF SEQUENCES:  22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Fish & Richardson P.C.
; STREET:  225 Franklin Street
; CITY:  Boston
; STATE:  MA
; COUNTRY:  USA
; ZIP:  02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/488,105
; FILING DATE:  07-JUN-1995

```

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 00537/112001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: The side chains of Lys at
; OTHER INFORMATION: position 26 and Asp at position 30 are linked by an
amide bond,
; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e.,
CONH2), rather
; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
US-08-488-105-7

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 22

US-08-468-275-6

```

; Sequence 6, Application US/08468275
; Patent No. 5747453
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/468,275
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 496-8150
; TELEFAX: (415) 496-8048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-275-6

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 23

```

US-08-449-500-1
; Sequence 1, Application US/08449500
; Patent No. 5798225
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,500
; FILING DATE: 18-JAN-1994

```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-500-1

```

```

Query Match          100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 24

```

US-08-449-317A-1
; Sequence 1, Application US/08449317A
; Patent No. 5807823
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,317A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-317A-1

Query Match 100.0%; Score 30; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 25

US-08-142-551B-2

; Sequence 2, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "The sequence of the 34
; OTHER INFORMATION: amino acid truncated human PTH peptide,
; OTHER INFORMATION: designated: Human PTH."
US-08-142-551B-2

```

```

Query Match          100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 26

```

US-08-477-022-1
; Sequence 1, Application US/08477022
; Patent No. 5821225
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,022
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796

```

; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-477-022-1

Query Match 100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 27

US-08-449-447-1

; Sequence 1, Application US/08449447
; Patent No. 5840837
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,447
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-447-1

Query Match 100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 28

US-08-835-231-13

; Sequence 13, Application US/08835231
; Patent No. 5861284

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 5861284uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,231
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991

```

; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-835-231-13

```

```

Query Match          100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 29

US-08-184-328-1

```

; Sequence 1, Application US/08184328
; Patent No. 5874086
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,328
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-184-328-1
```

```
Query Match          100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
```

```
RESULT 30
US-08-411-726-2
; Sequence 2, Application US/08411726
; Patent No. 5880093
; GENERAL INFORMATION:
; APPLICANT: BAGNOLI, Franco
; TITLE OF INVENTION: Use of Parathormone, Its Biologically
; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The
Preparation of
; TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment
of Pregnanc
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1 Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: WordPerfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,726
```

```

; FILING DATE: 05-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/02755
; FILING DATE: 08-OCT-1993
; APPLICATION NUMBER: MI-92A002331
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PALMESE, Maria Luisa
; REGISTRATION NUMBER: 34,402
; REFERENCE/DOCKET NUMBER: 2111/1300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-425-7200
; TELEFAX: 212-425-5288
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-411-726-2

```

```

Query Match          100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 31

```

US-08-691-647C-5
; Sequence 5, Application US/08691647C
; Patent No. 5955425
; GENERAL INFORMATION:
; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE, P.C.
; STREET: 1100 New York Avenue, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,647C
; FILING DATE: August 2, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4005
; TELEFAX: (703) 816-4100
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-647C-5

```

```

Query Match          100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 32

```

US-08-521-097-1
; Sequence 1, Application US/08521097
; Patent No. 5977070
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/521,097
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,328
; FILING DATE: 18-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-521-097-1

```

```

Query Match          100.0%; Score 30; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 33

US-09-044-536A-1

```

; Sequence 1, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A

```

```

; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-1

```

```

Query Match          100.0%; Score 30; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

```

RESULT 34
US-08-904-760B-22
; Sequence 22, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-904-760B-22

```

```

Query Match          100.0%; Score 30; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

```

RESULT 35
US-08-903-497A-1
; Sequence 1, Application US/08903497A
; Patent No. 6147186
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: J ppner, Harald
; TITLE OF INVENTION: No. 6147186el Parathyroid Hormone-Related
; TITLE OF INVENTION: Peptide Analogs
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/903,497A
; FILING DATE: 30-JUL-1997

```



```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,471
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: MODIFIED-SITE
; LOCATION: 34
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
; OTHER INFORMATION: AMIDE
US-08-903-497A-1

```

```

Query Match          100.0%; Score 30; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 36

US-09-108-661-13

```

; Sequence 13, Application US/09108661
; Patent No. 6287806

```

GENERAL INFORMATION:

```

; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 6287806uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,661
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-09-108-661-13

```

```

Query Match          100.0%; Score 30; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 37

US-09-007-466-6

; Sequence 6, Application US/09007466

; Patent No. 6313092

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.

; APPLICANT: OLDENBURG, KEVIN R.

; TITLE OF INVENTION: METHOD FOR INCREASING THE

; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALZA CORPORATION

; STREET: 950 PAGE MILL ROAD

```

; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,466
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,275
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: O360-0002; ARC-2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 496-8150
; TELEFAX: (415) 496-8048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-007-466-6

```

```

Query Match          100.0%; Score 30; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 38

US-09-406-813-1

```

; Sequence 1, Application US/09406813
; Patent No. 6316410
; GENERAL INFORMATION:
; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 10688-1B
; CURRENT APPLICATION NUMBER: US/09/406,813
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01

```

```
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 1
;  LENGTH: 34
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-406-813-1
```

Query Match 100.0%; Score 30; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 39

US-08-952-980B-6

; Sequence 6, Application US/08952980B

; Patent No. 6333189

; GENERAL INFORMATION:

APPLICANT: HOLLADAY, LESLIE A.

APPLICANT: OLDENBURG, KEVIN R.

TITLE OF INVENTION: METHOD FOR INCREASING THE

TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

ADDRESSEE: ALZA CORPORATION

STREET: 950 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94303-0802

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/952,980B

FILING DATE: 20-NOV-1997

; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: MILLER, D. BYRON

REGISTRATION NUMBER: 3

REFERENCE/DOCKET NUMBER: 23

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 496-8150

TELEFAX: (650) 496-8048

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

```
;      TYPE:  amino acid
```

```
; STRANDEDNESS: single
```

```
;      TOPOLOGY:  linear
```

; MOLECULE TYPE: protein

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 8.8785 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-166
Perfect score: 30
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	5	16.7	34	2	A84241	hypothetical prote
2	5	16.7	34	2	B97032	transcription regu
3	5	16.7	35	2	E95098	hypothetical prote
4	4	13.3	28	2	T09594	gene LFY protein -
5	4	13.3	29	1	A55527	pyrroloquinoline q
6	4	13.3	29	2	S01614	dystrophin - rat (
7	4	13.3	29	2	I78537	copper transportin
8	4	13.3	29	2	S78412	ribosomal protein
9	4	13.3	30	2	S63531	hypothetical prote
10	4	13.3	31	2	S44471	glucagon G1 - Nort
11	4	13.3	31	2	S44472	glucagon G2 - Nort
12	4	13.3	31	2	D70236	hypothetical prote
13	4	13.3	32	2	F23454	ovalbumin phosphos

14	4	13.3	32	2	D31461	T-cell receptor de
15	4	13.3	32	2	G84161	hypothetical prote
16	4	13.3	33	2	E81714	hypothetical prote
17	4	13.3	35	2	D23454	ovalbumin phosphos
18	4	13.3	35	2	G23454	ovalbumin phosphos
19	4	13.3	35	2	D82125	hypothetical prote
20	4	13.3	36	2	S70806	hypothetical prote
21	4	13.3	36	2	F95057	hypothetical prote
22	4	13.3	36	2	A84774	hypothetical prote
23	4	13.3	36	2	S46227	hypothetical prote
24	4	13.3	37	2	S71912	hemoglobin, extrac
25	4	13.3	37	2	T12635	homeotic protein H
26	4	13.3	39	1	CKFHCS	sarcotoxin IC - fl
27	4	13.3	39	2	S71913	hemoglobin, extrac
28	3	10.0	28	2	A42272	brain-type creatin
29	3	10.0	28	2	C32416	phospholipase A2 (
30	3	10.0	28	2	B60071	vasoactive intesti
31	3	10.0	28	2	A60304	vasoactive intesti
32	3	10.0	28	2	S58386	T-cell receptor be
33	3	10.0	28	2	PN0047	signal transductio
34	3	10.0	28	2	S70894	hypothetical prote
35	3	10.0	28	2	S22469	hypothetical prote
36	3	10.0	28	2	S26254	rel protein - chic
37	3	10.0	28	2	I59477	antigen, T-cell re
38	3	10.0	28	2	F46522	T-cell receptor et
39	3	10.0	28	2	H85908	hypothetical prote
40	3	10.0	29	1	GCCB	glucagon - Chinch
41	3	10.0	29	2	S39968	probable hydro-lya
42	3	10.0	29	2	A61509	islet amyloid poly
43	3	10.0	29	2	S17147	galanin - chicken
44	3	10.0	29	2	T44245	ribosomal protein
45	3	10.0	29	2	A05272	gelsolin, cytosoli
46	3	10.0	29	2	B44101	calmodulin, vasoac
47	3	10.0	29	2	S42642	probable rhicadhes
48	3	10.0	29	2	B81136	hypothetical prote
49	3	10.0	29	2	I84189	cyclic AMP recepto
50	3	10.0	29	2	S65747	CDP-paratose synth
51	3	10.0	29	2	S65748	CDP-paratose synth
52	3	10.0	29	2	B41476	probable antigen 2
53	3	10.0	29	2	S68094	2,3-dihydroxybenzo
54	3	10.0	29	2	A27688	mammary-derived gr
55	3	10.0	29	2	T31443	cytochrome bc chai
56	3	10.0	29	2	F85570	hypothetical prote
57	3	10.0	29	2	I49732	NADH2 dehydrogenas
58	3	10.0	29	2	A59479	NADP phosphatase I
59	3	10.0	30	2	S40309	tyrosine 3-monooxy
60	3	10.0	30	2	C21897	ornithine carbamoy
61	3	10.0	30	2	A28562	glutathione transf
62	3	10.0	30	2	A05315	pancreatic ribonuc
63	3	10.0	30	2	A44598	endo-1,4-beta-xyla
64	3	10.0	30	2	A61333	trypsin (EC 3.4.21
65	3	10.0	30	2	S21815	H+-exporting ATPas
66	3	10.0	30	2	A44912	cysteine proteinas
67	3	10.0	30	2	B61125	glucagon-like pept
68	3	10.0	30	2	C61125	glucagon-like pept
69	3	10.0	30	2	F32502	T-cell receptor de
70	3	10.0	30	2	PD0013	cAMP response elem

71	3	10.0	30	2	S21195	spectrin beta chain
72	3	10.0	30	2	PC4172	profilin - rat (fr
73	3	10.0	30	2	A34461	heat shock protein
74	3	10.0	30	2	A22977	delta-endotoxin -
75	3	10.0	30	2	A44913	34K core flagella
76	3	10.0	30	2	S08565	ribulose-bisphosph
77	3	10.0	30	2	S30333	N-carbamoyl-D-amin
78	3	10.0	30	2	PQ0444	hypothetical prote
79	3	10.0	30	2	H95021	hypothetical prote
80	3	10.0	30	2	D72276	hypothetical prote
81	3	10.0	30	2	D70253	conserved hypothet
82	3	10.0	30	2	B70165	hypothetical prote
83	3	10.0	30	2	B81956	hypothetical prote
84	3	10.0	30	2	E82294	hypothetical prote
85	3	10.0	30	2	S72626	small-cell-variant
86	3	10.0	30	2	A35687	probable 39K inorg
87	3	10.0	30	2	S73316	photosystem I chain
88	3	10.0	30	2	A32946	trypsin-like serin
89	3	10.0	30	2	PL0189	Ig light chain - s
90	3	10.0	30	2	S65519	carcinoembryonic a
91	3	10.0	30	2	S34765	4-hydroxybutyryl-C
92	3	10.0	30	2	D81532	hypothetical prote
93	3	10.0	30	2	A48923	retrovirus-related
94	3	10.0	30	2	B56586	storage hexamer 2
95	3	10.0	30	2	F81360	very hypothetical
96	3	10.0	30	2	S15650	NADH2 dehydrogenas
97	3	10.0	30	2	H97596	hypothetical prote
98	3	10.0	30	4	I52605	hypothetical MLL/E
99	3	10.0	31	1	A28805	leiurotoxin I [val
100	3	10.0	31	1	A49078	leiurotoxin I-like
101	3	10.0	31	1	S34504	photosystem I prot
102	3	10.0	31	2	T44925	hypothetical prote
103	3	10.0	31	2	S39019	glucagon-like pept
104	3	10.0	31	2	A58793	relaxin chain B -
105	3	10.0	31	2	A58586	conotoxin MrVIA -
106	3	10.0	31	2	F30608	Ig kappa chain V-I
107	3	10.0	31	2	D30608	Ig kappa chain V-I
108	3	10.0	31	2	F31461	T-cell receptor de
109	3	10.0	31	2	I52232	tau protein - huma
110	3	10.0	31	2	A36162	neutrophil-activat
111	3	10.0	31	2	S04980	ferritin heavy cha
112	3	10.0	31	2	S32610	antiviral protein
113	3	10.0	31	2	S38881	inner membrane pro
114	3	10.0	31	2	G95018	hypothetical prote
115	3	10.0	31	2	G95022	hypothetical prote
116	3	10.0	31	2	A95085	hypothetical prote
117	3	10.0	31	2	H95093	hypothetical prote
118	3	10.0	31	2	E95140	hypothetical prote
119	3	10.0	31	2	E95151	hypothetical prote
120	3	10.0	31	2	E70202	hypothetical prote
121	3	10.0	31	2	E70223	hypothetical prote
122	3	10.0	31	2	H70225	hypothetical prote
123	3	10.0	31	2	C70240	hypothetical prote
124	3	10.0	31	2	E64562	hypothetical prote
125	3	10.0	31	2	S49191	hypothetical prote
126	3	10.0	31	2	H82353	hypothetical prote
127	3	10.0	31	2	A05051	hypothetical prote

128	3	10.0	31	2	B23605	histone H1.3 - whe
129	3	10.0	31	2	S78738	protein YOL038c-a
130	3	10.0	31	2	A36221	cecropin P1 - pig
131	3	10.0	31	2	S27112	sarcophilin - rabbi
132	3	10.0	31	2	D81591	hypothetical prote
133	3	10.0	31	2	G81558	hypothetical prote
134	3	10.0	31	2	G82816	hypothetical prote
135	3	10.0	31	2	F82565	hypothetical prote
136	3	10.0	32	1	TCEE	calcitonin - Japan
137	3	10.0	32	1	TCON2	calcitonin 2 - soc
138	3	10.0	32	1	TCON2C	calcitonin 2 - chu
139	3	10.0	32	1	TCON2P	calcitonin 2 - pin
140	3	10.0	32	1	TCON3	calcitonin 3 - coh
141	3	10.0	32	2	S20719	alcohol dehydrogen
142	3	10.0	32	2	A61143	trypsin (EC 3.4.21
143	3	10.0	32	2	D32502	T-cell receptor de
144	3	10.0	32	2	A32502	T-cell receptor de
145	3	10.0	32	2	B40186	ubiquitin / riboso
146	3	10.0	32	2	S57780	histone H3 - rice
147	3	10.0	32	2	A24047	gap junction prote
148	3	10.0	32	2	S51524	anchorin CII - bov
149	3	10.0	32	2	S36809	GTP-binding regula
150	3	10.0	32	2	A29743	translation initia
151	3	10.0	32	2	A03367	lectin - Macrotylo
152	3	10.0	32	2	A44900	fimbrin, SEF 21 -
153	3	10.0	32	2	S03273	photosystem II oxy
154	3	10.0	32	2	C46107	polyomavirus enhan
155	3	10.0	32	2	S08482	regulatory protein
156	3	10.0	32	2	E87694	hypothetical prote
157	3	10.0	32	2	D70222	hypothetical prote
158	3	10.0	32	2	E70225	hypothetical prote
159	3	10.0	32	2	B70241	hypothetical prote
160	3	10.0	32	2	B70257	hypothetical prote
161	3	10.0	32	2	E82279	hypothetical prote
162	3	10.0	32	2	E82089	hypothetical prote
163	3	10.0	32	2	H82416	hypothetical prote
164	3	10.0	32	2	T17394	vrlN protein - Dic
165	3	10.0	32	2	S23476	hypothetical prote
166	3	10.0	32	2	S22304	hypothetical prote
167	3	10.0	32	2	S78323	photosystem II pro
168	3	10.0	32	2	A05015	hypothetical prote
169	3	10.0	32	2	I38619	zinc finger protei
170	3	10.0	32	2	S28398	t-complex protein
171	3	10.0	32	2	T14569	hypothetical prote
172	3	10.0	32	2	H84081	hypothetical prote
173	3	10.0	32	2	F82833	hypothetical prote
174	3	10.0	32	2	JC5802	ovulation stimulat
175	3	10.0	32	2	E85588	hypothetical prote
176	3	10.0	33	2	S43312	2',3'-cyclic-nucle
177	3	10.0	33	2	S26859	chitinase (EC 3.2.
178	3	10.0	33	2	I52219	c-ras-Ki-2 protein
179	3	10.0	33	2	I53221	K-ras protein - hu
180	3	10.0	33	2	PC2300	gaegurin 1 - Korea
181	3	10.0	33	2	I56451	relaxin - hamadrya
182	3	10.0	33	2	E32502	T-cell receptor de
183	3	10.0	33	2	A31461	T-cell receptor de
184	3	10.0	33	2	B31461	T-cell receptor de

185	3	10.0	33	2	A03150	retinoic acid-bind
186	3	10.0	33	2	C46027	neurotransmitter t
187	3	10.0	33	2	PQ0150	dnaK-type molecula
188	3	10.0	33	2	B44906	L1 protein - human
189	3	10.0	33	2	PQ0418	matrix protein M1
190	3	10.0	33	2	S34505	hypothetical prote
191	3	10.0	33	2	G95006	hypothetical prote
192	3	10.0	33	2	C95200	hypothetical prote
193	3	10.0	33	2	A87213	hypothetical prote
194	3	10.0	33	2	F84163	hypothetical prote
195	3	10.0	33	2	E82135	hypothetical prote
196	3	10.0	33	2	H82475	hypothetical prote
197	3	10.0	33	2	S68096	lactate dehydrogen
198	3	10.0	33	2	E82526	hypothetical prote
199	3	10.0	33	2	AC1012	hypothetical prote
200	3	10.0	33	2	C97406	hypothetical prote
201	3	10.0	34	2	S57282	phospholipase A2 (
202	3	10.0	34	2	A40298	dermaseptin - Sauv
203	3	10.0	34	2	JS0426	big gastrin - goat
204	3	10.0	34	2	I48887	cryptdin-4 - mouse
205	3	10.0	34	2	I32502	T-cell receptor de
206	3	10.0	34	2	H31461	T-cell receptor de
207	3	10.0	34	2	A19197	class II histocomp
208	3	10.0	34	2	D48147	troponin I (altern
209	3	10.0	34	2	A43564	neurogenic protein
210	3	10.0	34	2	H95047	hypothetical prote
211	3	10.0	34	2	D95189	hypothetical prote
212	3	10.0	34	2	C90973	hypothetical prote
213	3	10.0	34	2	F70242	hypothetical prote
214	3	10.0	34	2	B70252	hypothetical prote
215	3	10.0	34	2	F81919	hypothetical prote
216	3	10.0	34	2	H81883	hypothetical prote
217	3	10.0	34	2	F81044	hypothetical prote
218	3	10.0	34	2	F82163	hypothetical prote
219	3	10.0	34	2	E82100	hypothetical prote
220	3	10.0	34	2	B82449	hypothetical prote
221	3	10.0	34	2	S13662	cellulase (EC 3.2.
222	3	10.0	34	2	A60110	repetitive protein
223	3	10.0	34	2	S44828	F54F2.3 protein -
224	3	10.0	34	2	S40662	P-cadherin - mouse
225	3	10.0	34	2	F84079	hypothetical prote
226	3	10.0	34	2	H81600	hypothetical prote
227	3	10.0	34	2	H82820	hypothetical prote
228	3	10.0	34	2	C82819	hypothetical prote
229	3	10.0	34	2	B82679	hypothetical prote
230	3	10.0	34	2	G85820	unknown protein en
231	3	10.0	34	2	S12554	hydroxymethylgluta
232	3	10.0	35	2	E38601	Ig kappa chain V r
233	3	10.0	35	2	A05302	hemoglobin beta ch
234	3	10.0	35	2	A29663	histone H4 - starf
235	3	10.0	35	2	S27154	ribosomal protein
236	3	10.0	35	2	E48401	ribosomal protein
237	3	10.0	35	2	S13435	lectin III - furze
238	3	10.0	35	2	S74556	photosystem II psb
239	3	10.0	35	2	S18224	filamentous hemagg
240	3	10.0	35	2	S18226	opacity protein op
241	3	10.0	35	2	T07870	major latex protei

242	3	10.0	35	2	B33770	hypothetical prote
243	3	10.0	35	2	PS0439	potassium channel
244	3	10.0	35	2	I48925	homeobox protein -
245	3	10.0	35	2	F87622	hypothetical prote
246	3	10.0	35	2	C96619	protein T30E16.7 [
247	3	10.0	35	2	B84674	hypothetical prote
248	3	10.0	35	2	F84395	hypothetical prote
249	3	10.0	35	2	B82012	hypothetical prote
250	3	10.0	35	2	H81948	hypothetical prote
251	3	10.0	35	2	A82151	hypothetical prote
252	3	10.0	35	2	F82051	hypothetical prote
253	3	10.0	35	2	S58708	neutral phosphatas
254	3	10.0	35	2	F69827	hypothetical prote
255	3	10.0	35	2	C69977	hypothetical prote
256	3	10.0	35	2	S65772	early nodulin 40 -
257	3	10.0	35	2	A38107	mammalian toxin -
258	3	10.0	35	2	S49309	oncofetal protein
259	3	10.0	35	2	C81560	hypothetical prote
260	3	10.0	36	2	H32502	T-cell receptor de
261	3	10.0	36	2	C32502	T-cell receptor de
262	3	10.0	36	2	S08552	ribosomal protein
263	3	10.0	36	2	S72299	ribosomal protein
264	3	10.0	36	2	B44400	myosin heavy chain
265	3	10.0	36	2	I46593	myosin - pig (frag
266	3	10.0	36	2	B31872	retinoic acid-bind
267	3	10.0	36	2	S35572	zona pellucida pro
268	3	10.0	36	2	B41481	virulence-associat
269	3	10.0	36	2	A38659	methanol dehydroge
270	3	10.0	36	2	C95218	conserved domain p
271	3	10.0	36	2	E84416	hypothetical prote
272	3	10.0	36	2	S17834	acetyl-CoA carboxy
273	3	10.0	36	2	E70220	hypothetical prote
274	3	10.0	36	2	E70238	hypothetical prote
275	3	10.0	36	2	F64604	hypothetical prote
276	3	10.0	36	2	G81853	hypothetical prote
277	3	10.0	36	2	S16552	hypothetical prote
278	3	10.0	36	2	G82281	hypothetical prote
279	3	10.0	36	2	A82163	hypothetical prote
280	3	10.0	36	2	C82111	hypothetical prote
281	3	10.0	36	2	A82092	hypothetical prote
282	3	10.0	36	2	B82093	hypothetical prote
283	3	10.0	36	2	A82437	hypothetical prote
284	3	10.0	36	2	A38729	pyruvate decarboxy
285	3	10.0	36	2	A69326	hypothetical prote
286	3	10.0	36	2	S67795	probable membrane
287	3	10.0	36	2	T22263	hypothetical prote
288	3	10.0	36	2	A57443	guanylate cyclase
289	3	10.0	36	2	D83682	hypothetical prote
290	3	10.0	36	2	A83870	hypothetical prote
291	3	10.0	36	2	F84074	hypothetical prote
292	3	10.0	36	2	A56634	neuropeptide F - A
293	3	10.0	36	2	S77071	probable plastoqui
294	3	10.0	36	2	AF1015	hypothetical prote
295	3	10.0	36	2	AI1841	hypothetical prote
296	3	10.0	37	1	S32792	iberiotoxin - east
297	3	10.0	37	1	HSWT93	histone H2A.3 - wh
298	3	10.0	37	2	S48656	fusicoccin recepto

299	3	10.0	37	2	S03570	trypsin (EC 3.4.21
300	3	10.0	37	2	S39367	proteinase omega -
301	3	10.0	37	2	S06217	transforming prote
302	3	10.0	37	2	S05037	insulinoma amyloid
303	3	10.0	37	2	A30607	Ig kappa chain V-I
304	3	10.0	37	2	PC1121	antifungal 25K pro
305	3	10.0	37	2	G01887	MEK kinase - human
306	3	10.0	37	2	S07517	gene 6.3 protein -
307	3	10.0	37	2	G70223	hypothetical prote
308	3	10.0	37	2	E70241	hypothetical prote
309	3	10.0	37	2	D83199	hypothetical prote
310	3	10.0	37	2	H82304	hypothetical prote
311	3	10.0	37	2	S21132	photosystem II cyt
312	3	10.0	37	2	F59103	hypothetical prote
313	3	10.0	37	2	T36662	small hypothetical
314	3	10.0	37	2	T11815	hypothetical prote
315	3	10.0	37	2	A57127	diuretic hormone 1
316	3	10.0	37	2	C32112	R15 gamma peptide
317	3	10.0	37	2	B48845	sterol regulatory
318	3	10.0	37	2	S68261	hypothetical prote
319	3	10.0	37	2	S49982	Tcell receptor alp
320	3	10.0	37	2	B39030	androgen-binding p
321	3	10.0	37	2	PN0550	metabotropic gluta
322	3	10.0	37	2	S70931	histone-like prote
323	3	10.0	37	2	F81403	hypothetical prote
324	3	10.0	38	1	R5EC36	ribosomal protein
325	3	10.0	38	2	C34047	stylar glycoprotei
326	3	10.0	38	2	T11763	acetyl-CoA carboxy
327	3	10.0	38	2	S39034	lipid transfer pro
328	3	10.0	38	2	A42974	natriuretic peptid
329	3	10.0	38	2	A49165	pituitary adenylat
330	3	10.0	38	2	A61070	pituitary adenylat
331	3	10.0	38	2	PS0129	H-2 class I histoc
332	3	10.0	38	2	S50764	ribosomal protein
333	3	10.0	38	2	E72247	ribosomal protein
334	3	10.0	38	2	H83113	50S ribosomal prot
335	3	10.0	38	2	AG0028	50S ribosomal prot
336	3	10.0	38	2	D91149	50S ribosomal subu
337	3	10.0	38	2	AF1008	50S ribosomal chai
338	3	10.0	38	2	PH1920	annexin-like 40K p
339	3	10.0	38	2	S72344	pile protein - Nei
340	3	10.0	38	2	A60216	hyperglycemic horm
341	3	10.0	38	2	S65416	pyruvate synthase
342	3	10.0	38	2	B95069	hypothetical prote
343	3	10.0	38	2	A95139	hypothetical prote
344	3	10.0	38	2	H91111	hypothetical prote
345	3	10.0	38	2	D90631	hypothetical prote
346	3	10.0	38	2	E72306	hypothetical prote
347	3	10.0	38	2	E81873	hypothetical prote
348	3	10.0	38	2	T14885	hypothetical prote
349	3	10.0	38	2	A82478	hypothetical prote
350	3	10.0	38	2	E82463	hypothetical prote
351	3	10.0	38	2	A82450	hypothetical prote
352	3	10.0	38	2	D37842	hypothetical prote
353	3	10.0	38	2	B69492	hypothetical prote
354	3	10.0	38	2	S23173	photosystem I chai
355	3	10.0	38	2	T01992	hypothetical prote

356	3	10.0	38	2	S58601	hypothetical prote
357	3	10.0	38	2	T01741	hypothetical prote
358	3	10.0	38	2	B39888	synapsin I - bovin
359	3	10.0	38	2	B49012	orf 5' of megl - m
360	3	10.0	38	2	A83863	hypothetical prote
361	3	10.0	38	2	H81603	hypothetical prote
362	3	10.0	38	2	E82858	hypothetical prote
363	3	10.0	38	2	G71305	probable ribosomal
364	3	10.0	38	2	B97327	hypothetical prote
365	3	10.0	38	2	E86077	hypothetical prote
366	3	10.0	38	2	H85994	50S ribosomal subu
367	3	10.0	38	2	T08652	hypothetical prote
368	3	10.0	38	2	AB0747	hypothetical prote
369	3	10.0	38	2	AH0774	hypothetical prote
370	3	10.0	38	2	C97551	hypothetical prote
371	3	10.0	39	1	CTDFAS	corticotropin - sp
372	3	10.0	39	1	HWGH3Z	exendin-3 - Mexica
373	3	10.0	39	1	HWGH4G	exendin-4 - Gila m
374	3	10.0	39	2	B45946	gamma-glutamyltran
375	3	10.0	39	2	I55325	aspartate transami
376	3	10.0	39	2	S09645	hygromycin-B kinas
377	3	10.0	39	2	A01458	corticotropin - fi
378	3	10.0	39	2	PN0127	corticotropin - se
379	3	10.0	39	2	A61127	adrenocorticotropi
380	3	10.0	39	2	A01459	corticotropin - os
381	3	10.0	39	2	A01457	corticotropin - ra
382	3	10.0	39	2	C55995	prostaglandin E2 r
383	3	10.0	39	2	S07458	Ig kappa chain V r
384	3	10.0	39	2	PH0878	Ig kappa chain V r
385	3	10.0	39	2	S72459	ribosomal protein
386	3	10.0	39	2	PQ0011	tubulin beta chain
387	3	10.0	39	2	S63482	tubulin beta chain
388	3	10.0	39	2	A45793	actin - nematode (
389	3	10.0	39	2	AH2286	photosystem II pro
390	3	10.0	39	2	S77164	ycf32 protein - Sy
391	3	10.0	39	2	G64944	yebJ protein - Esc
392	3	10.0	39	2	A85795	hypothetical prote
393	3	10.0	39	2	S78008	fucosyltransferase
394	3	10.0	39	2	A48110	RNA recognition mo
395	3	10.0	39	2	H95146	hypothetical prote
396	3	10.0	39	2	D70239	hypothetical prote
397	3	10.0	39	2	C70254	hypothetical prote
398	3	10.0	39	2	G81899	hypothetical prote
399	3	10.0	39	2	B81912	hypothetical prote
400	3	10.0	39	2	B81954	very hypothetical
401	3	10.0	39	2	F82329	hypothetical prote
402	3	10.0	39	2	A43591	43K outer membrane
403	3	10.0	39	2	A44918	lactococcin G pept
404	3	10.0	39	2	S67938	hypothetical prote
405	3	10.0	39	2	S73118	photosystem II pro
406	3	10.0	39	2	PC4294	high mobility grou
407	3	10.0	39	2	T15158	hypothetical prote
408	3	10.0	39	2	I46466	luteinizing hormon
409	3	10.0	39	2	B40984	finger protein zfe
410	3	10.0	39	2	T03365	gene e2 protein -
411	3	10.0	39	2	F81587	hypothetical prote
412	3	10.0	39	2	E81540	hypothetical prote

413	3	10.0	39	2	T12905	hypothetical prote
414	3	10.0	39	2	AD0162	hypothetical prote
415	3	10.0	39	2	AE3109	hypothetical prote
416	3	10.0	40	1	SWFGS	sauvagine - Sauvag
417	3	10.0	40	2	B61320	plastocyanin - Aqu
418	3	10.0	40	2	S52343	hypothetical prote
419	3	10.0	40	2	S00264	creatine kinase (E
420	3	10.0	40	2	S34407	adenylate kinase (
421	3	10.0	40	2	PQ0202	endo-1,4-beta-xyla
422	3	10.0	40	2	S50021	trypsin-like prote
423	3	10.0	40	2	B60908	beta-lactamase (EC
424	3	10.0	40	2	B41440	protein disulfide-
425	3	10.0	40	2	A19940	antithrombin III -
426	3	10.0	40	2	B59005	thymosin beta - sc
427	3	10.0	40	2	A59005	thymosin beta - se
428	3	10.0	40	2	B31791	sarcotoxin ID - fl
429	3	10.0	40	2	S07969	T-cell receptor al
430	3	10.0	40	2	I50012	MHC class I protei
431	3	10.0	40	2	I50013	MHC class I protei
432	3	10.0	40	2	S61539	ribosomal protein
433	3	10.0	40	2	A60171	proteoglycan core
434	3	10.0	40	2	A60645	tubulin beta chain
435	3	10.0	40	2	A29184	vitellogenin - tur
436	3	10.0	40	2	S65907	conglutin gamma -
437	3	10.0	40	2	S08656	protein VI - human
438	3	10.0	40	2	A53708	indolepyruvate syn
439	3	10.0	40	2	T08107	nonenzymatic prote
440	3	10.0	40	2	S71917	hemoglobin, extrac
441	3	10.0	40	2	S58853	homeotic protein u
442	3	10.0	40	2	H95063	hypothetical prote
443	3	10.0	40	2	H91281	hypothetical prote
444	3	10.0	40	2	A87642	hypothetical prote
445	3	10.0	40	2	F87419	hypothetical prote
446	3	10.0	40	2	C32338	hypothetical 4K pr
447	3	10.0	40	2	C72398	hypothetical prote
448	3	10.0	40	2	S44935	hypothetical prote
449	3	10.0	40	2	A82203	hypothetical prote
450	3	10.0	40	2	G82484	hypothetical prote
451	3	10.0	40	2	A82382	hypothetical prote
452	3	10.0	40	2	I39944	regulatory extrace
453	3	10.0	40	2	F69677	phosphatase (RapK)
454	3	10.0	40	2	I41476	probable antigen 9
455	3	10.0	40	2	S27709	hypothetical prote
456	3	10.0	40	2	F45095	photosystem I ligh
457	3	10.0	40	2	T11811	hypothetical prote
458	3	10.0	40	2	T07472	hypothetical prote
459	3	10.0	40	2	T07516	hypothetical prote
460	3	10.0	40	2	T07523	hypothetical prote
461	3	10.0	40	2	T07560	hypothetical prote
462	3	10.0	40	2	T48629	hypothetical prote
463	3	10.0	40	2	S53001	mitotic-specific c
464	3	10.0	40	2	T03831	hypothetical prote
465	3	10.0	40	2	S71295	deoxyguanosine kin
466	3	10.0	40	2	S56768	capsid protein - L
467	3	10.0	40	2	T07206	hypothetical prote
468	3	10.0	40	2	H81592	hypothetical prote
469	3	10.0	40	2	H81520	hypothetical prote

470	3	10.0	40	2	F81511	hypothetical prote
471	3	10.0	40	2	G82620	hypothetical prote
472	3	10.0	40	2	A82590	hypothetical prote
473	3	10.0	40	2	A86123	hypothetical prote
474	3	10.0	40	2	B97413	hypothetical prote
475	2	6.7	28	1	LFSEW	trp operon leader
476	2	6.7	28	1	LFEBLT	leu operon leader
477	2	6.7	28	1	LFECL	leu operon leader
478	2	6.7	28	1	G9BPSV	gene 9 protein - s
479	2	6.7	28	2	S41774	ubiquinol-cytochro
480	2	6.7	28	2	S71598	cytochrome P450 HP
481	2	6.7	28	2	S04341	cytochrome P450 PB
482	2	6.7	28	2	PX0033	cytochrome P450 te
483	2	6.7	28	2	S66436	allophycocyanin al
484	2	6.7	28	2	S47624	D-aspartate oxidas
485	2	6.7	28	2	T14210	NADH2 dehydrogenas
486	2	6.7	28	2	T14213	NADH2 dehydrogenas
487	2	6.7	28	2	T12301	NADH2 dehydrogenas
488	2	6.7	28	2	PC1162	cytochrome-c oxida
489	2	6.7	28	2	S21278	glutathione transf
490	2	6.7	28	2	C33948	glutathione transf
491	2	6.7	28	2	A34244	hexokinase (EC 2.7
492	2	6.7	28	2	D38578	protein kinase 4 (
493	2	6.7	28	2	B39116	epidermal growth f
494	2	6.7	28	2	A31859	deoxycytidine kina
495	2	6.7	28	2	B54257	deoxynucleoside ki
496	2	6.7	28	2	I55596	lysosomal acid lip
497	2	6.7	28	2	B35948	phospholipase A2 (
498	2	6.7	28	2	C35948	phospholipase A2 (
499	2	6.7	28	2	A35115	hypothetical prote
500	2	6.7	28	2	A61281	lysozyme homolog A
501	2	6.7	28	2	A61529	chymotrypsin (EC 3
502	2	6.7	28	2	A60291	24K proteinase (EC
503	2	6.7	28	2	S08186	proteasome beta ch
504	2	6.7	28	2	S55729	orotidine-5'-monop
505	2	6.7	28	2	I40034	trpE protein - Bac
506	2	6.7	28	2	A32643	deoxyribodipyrimid
507	2	6.7	28	2	S77854	glutamate-tRNA lig
508	2	6.7	28	2	JX0059	serine proteinase
509	2	6.7	28	2	S07156	trypsin inhibitor
510	2	6.7	28	2	JX0058	trypsin inhibitor
511	2	6.7	28	2	B45041	trypsin inhibitor
512	2	6.7	28	2	S20393	trypsin inhibitor
513	2	6.7	28	2	A25802	2S seed storage pr
514	2	6.7	28	2	T47196	RAS protein [impor
515	2	6.7	28	2	A61322	somatostatin-28 -
516	2	6.7	28	2	B60583	glycoprotein hormo
517	2	6.7	28	2	A38232	vasoactive intesti
518	2	6.7	28	2	A60303	vasoactive intesti
519	2	6.7	28	2	JT0412	bombyxin-IV chain
520	2	6.7	28	2	A56366	intestinal trefoil
521	2	6.7	28	2	C44180	alpha-neurotoxin-l
522	2	6.7	28	2	C39327	long neurotoxin -
523	2	6.7	28	2	I32529	Ig lambda chain V
524	2	6.7	28	2	PC1001	Ig light chain V r
525	2	6.7	28	2	B47719	T-cell receptor al
526	2	6.7	28	2	D47719	T-cell receptor al

527	2	6.7	28	2	S58389	T-cell receptor be
528	2	6.7	28	2	PH0250	T-cell receptor Vb
529	2	6.7	28	2	PH0247	T-cell receptor Vb
530	2	6.7	28	2	A49829	T-cell receptor va
531	2	6.7	28	2	D49829	T-cell receptor va
532	2	6.7	28	2	PH1908	T-cell receptor al
533	2	6.7	28	2	D41912	T-cell receptor be
534	2	6.7	28	2	G47719	house-dust-mite-re
535	2	6.7	28	2	E49533	T-cell receptor be
536	2	6.7	28	2	I46921	gene Bota protein
537	2	6.7	28	2	S11618	ribosomal protein
538	2	6.7	28	2	S51060	ribosomal protein
539	2	6.7	28	2	S51067	ribosomal protein
540	2	6.7	28	2	S72460	ribosomal protein
541	2	6.7	28	2	S08569	ribosomal protein
542	2	6.7	28	2	S10052	ribosomal protein
543	2	6.7	28	2	S55442	beta A2 crystallin
544	2	6.7	28	2	A45626	beta 2-tubulin - n
545	2	6.7	28	2	S21231	calcium-binding pr
546	2	6.7	28	2	A23691	apolipoprotein C-I
547	2	6.7	28	2	A05296	fibrinogen alpha c
548	2	6.7	28	2	A61113	cellular retinol-b
549	2	6.7	28	2	B35577	cell adhesion rece
550	2	6.7	28	2	I48349	fibronectin - mous
551	2	6.7	28	2	A61233	retinol-binding pr
552	2	6.7	28	2	I45911	dnaK-type molecula
553	2	6.7	28	2	PQ0263	dnaK-type molecula
554	2	6.7	28	2	A03356	omega-gliadin - ei
555	2	6.7	28	2	A60359	pollen allergen DG
556	2	6.7	28	2	A60752	outer membrane pro
557	2	6.7	28	2	PQ0691	photosystem I 5.6K
558	2	6.7	28	2	G32351	34K class B flagel
559	2	6.7	28	2	S47614	zinc finger protei
560	2	6.7	28	2	S49924	stp protein (Baker
561	2	6.7	28	2	B39227	calcium channel pr
562	2	6.7	28	2	F54346	pyruvate synthase
563	2	6.7	28	2	A36153	major allergen Ole
564	2	6.7	28	2	B54127	dolichyl-diphospho
565	2	6.7	28	2	S56746	alpha-synuclein, N
566	2	6.7	28	2	I48178	orphan receptor -
567	2	6.7	28	2	PC4429	peroxisome prolife
568	2	6.7	28	2	PC4430	peroxisome prolife
569	2	6.7	28	2	S29135	aminopyrine N-deme
570	2	6.7	28	2	S29136	aminopyrine N-deme
571	2	6.7	28	2	PN0625	homeobox JRX prote
572	2	6.7	28	2	B56779	tetM 5'-region lea
573	2	6.7	28	2	JU0297	fruR-shl operon le
574	2	6.7	28	2	G90638	leu operon leader
575	2	6.7	28	2	C90639	fruR leader peptid
576	2	6.7	28	2	B47310	MHVS28AA - murine
577	2	6.7	28	2	E64656	hypothetical prote
578	2	6.7	28	2	B64669	hypothetical prote
579	2	6.7	28	2	S15235	hypothetical prote
580	2	6.7	28	2	C56262	uvrB 3'-region hyp
581	2	6.7	28	2	E81239	hypothetical prote
582	2	6.7	28	2	I60364	phosphorybosylpyro
583	2	6.7	28	2	S56121	type I DNA methylt

584	2	6.7	28	2	B39191	hypothetical prote
585	2	6.7	28	2	T17391	hypothetical prote
586	2	6.7	28	2	A56499	brevicin-27 - Lact
587	2	6.7	28	2	A41476	probable antigen 1
588	2	6.7	28	2	S16228	aryl acylamidase -
589	2	6.7	28	2	PS0106	2-phosphinomethylm
590	2	6.7	28	2	G69384	conserved hypothet
591	2	6.7	28	2	A69259	hypothetical prote
592	2	6.7	28	2	T06925	hypothetical prote
593	2	6.7	28	2	S38524	rRNA N-glycosidase
594	2	6.7	28	2	PQ0800	calmodulin antagon
595	2	6.7	28	2	T06340	ribosomal protein
596	2	6.7	28	2	T07599	hypothetical prote
597	2	6.7	28	2	PH0220	peroxidase (EC 1.1
598	2	6.7	28	2	JQ0272	hypothetical 3K pr
599	2	6.7	28	2	S46250	fatty-acid-binding
600	2	6.7	28	2	A44923	carboxypeptidase 3
601	2	6.7	28	2	S64701	hypothetical prote
602	2	6.7	28	2	T38041	similarity to yeas
603	2	6.7	28	2	A27261	proteinase inhibit
604	2	6.7	28	2	A61417	bdellin B-3 - medi
605	2	6.7	28	2	S06668	toxin-like protein
606	2	6.7	28	2	S07826	venom protein - Am
607	2	6.7	28	2	C34923	omega-agatoxin IIA
608	2	6.7	28	2	A44877	cell surface prote
609	2	6.7	28	2	JW0019	mast cell degranul
610	2	6.7	28	2	A61273	interleukin-1 - st
611	2	6.7	28	2	S68643	nicotinic acetylch
612	2	6.7	28	2	PC2162	angiotensin II rec
613	2	6.7	28	2	I54183	cell adhesion regu
614	2	6.7	28	2	S54338	cytochrome P450 CY
615	2	6.7	28	2	I52627	erythrocyte chemok
616	2	6.7	28	2	JQ1035	hypothetical 3.2K
617	2	6.7	28	2	PH1335	Ig heavy chain DJ
618	2	6.7	28	2	S37683	protein IEF SSP 91
619	2	6.7	28	2	S37686	protein IEF SSP 92
620	2	6.7	28	2	PH1911	T-cell receptor al
621	2	6.7	28	2	I39288	ZF3 domain - human
622	2	6.7	28	2	PL0005	pepsin A (EC 3.4.2
623	2	6.7	28	2	A60692	proline-rich prote
624	2	6.7	28	2	PC2239	heat shock protein
625	2	6.7	28	2	PT0366	T-cell receptor be
626	2	6.7	28	2	I58115	cystic fibrosis tr
627	2	6.7	28	2	A46690	sialic acid-specif
628	2	6.7	28	2	C83797	hypothetical prote
629	2	6.7	28	2	C83969	hypothetical prote
630	2	6.7	28	2	S51593	myrB protein - Mic
631	2	6.7	28	2	C85490	fruR leader peptid
632	2	6.7	28	2	C97078	hypothetical prote
633	2	6.7	28	2	F97000	hypothetical prote
634	2	6.7	28	2	G85489	leu operon leader
635	2	6.7	28	2	AB1093	hypothetical prote
636	2	6.7	28	2	T06490	probable ribulose-
637	2	6.7	28	2	S73563	H+-transporting tw
638	2	6.7	28	2	AG0516	leu operon leader
639	2	6.7	28	4	I68614	frame shifted FMR1
640	2	6.7	28	4	JN0014	GABA(A) receptor a

641	2	6.7	29	1	TIPU	trypsin inhibitor
642	2	6.7	29	1	TIPU3	trypsin inhibitor
643	2	6.7	29	1	TIPU2B	trypsin inhibitor
644	2	6.7	29	1	GCOPV	glucagon - North A
645	2	6.7	29	1	GCDK	glucagon - duck
646	2	6.7	29	1	A61583	glucagon - ostrich
647	2	6.7	29	1	GCFLE	glucagon - Europea
648	2	6.7	29	1	GCDF	glucagon - smaller
649	2	6.7	29	1	GCEN	glucagon - elephan
650	2	6.7	29	1	GCTTS	glucagon - slider
651	2	6.7	29	1	TNLJBR	trans-activating t
652	2	6.7	29	1	Q1BP57	gene 1.5 protein -
653	2	6.7	29	2	A60558	cytochrome P450 HL
654	2	6.7	29	2	T17079	NADH2 dehydrogenas
655	2	6.7	29	2	T17076	NADH2 dehydrogenas
656	2	6.7	29	2	A48427	flavohemoglobin hm
657	2	6.7	29	2	A54234	cytochrome-c oxida
658	2	6.7	29	2	S08201	peroxidase (EC 1.1
659	2	6.7	29	2	A26208	acetyl-CoA C-acety
660	2	6.7	29	2	A22018	phosphotransferase
661	2	6.7	29	2	S46211	kallikrein rK8 (pK
662	2	6.7	29	2	S28174	heat-shock protein
663	2	6.7	29	2	A32414	bothrolysin (EC 3.
664	2	6.7	29	2	S17432	H+-transporting tw
665	2	6.7	29	2	S02578	H+-transporting tw
666	2	6.7	29	2	S23122	peptidylprolyl iso
667	2	6.7	29	2	JU0211	squash-type trypsi
668	2	6.7	29	2	T03653	phospholipid trans
669	2	6.7	29	2	C24536	alpha-amylase/tryp
670	2	6.7	29	2	C25310	alpha-amylase/tryp
671	2	6.7	29	2	D55998	brevinin-2Ed - edi
672	2	6.7	29	2	D53578	brevinin-2Ee - edi
673	2	6.7	29	2	A91740	glucagon - turkey
674	2	6.7	29	2	A91741	glucagon - rabbit
675	2	6.7	29	2	A91742	glucagon - Arabian
676	2	6.7	29	2	S07211	glucagon - marbled
677	2	6.7	29	2	A61135	glucagon - bigeye
678	2	6.7	29	2	C39258	glucagon - common
679	2	6.7	29	2	C60840	glucagon I - Europ
680	2	6.7	29	2	S39018	glucagon - bowfin
681	2	6.7	29	2	A39462	cholestokinin - do
682	2	6.7	29	2	A60791	toxin II.9 - scorp
683	2	6.7	29	2	JH0699	omega-conotoxin MV
684	2	6.7	29	2	A58537	omega-conotoxin MV
685	2	6.7	29	2	I52628	low affinity nerve
686	2	6.7	29	2	C61233	conceptus protein
687	2	6.7	29	2	S10061	Ig heavy chain (cl
688	2	6.7	29	2	PH0239	T-cell receptor Vb
689	2	6.7	29	2	PH0251	T-cell receptor Vb
690	2	6.7	29	2	PH0254	T-cell receptor Vb
691	2	6.7	29	2	PH0233	T-cell receptor Vb
692	2	6.7	29	2	E31485	Ig heavy chain V r
693	2	6.7	29	2	H31485	Ig kappa chain V r
694	2	6.7	29	2	G31461	T-cell receptor de
695	2	6.7	29	2	C47719	T-cell receptor al
696	2	6.7	29	2	E47719	house-dust-mite-re
697	2	6.7	29	2	PS0134	H-2 class I histoc

698	2	6.7	29	2	PS0132	H-2 class I histoc
699	2	6.7	29	2	I37534	gene HLA-DRB prote
700	2	6.7	29	2	I37535	gene HLA-DRB prote
701	2	6.7	29	2	I37536	MHC class II histo
702	2	6.7	29	2	I37301	MHC class II histo
703	2	6.7	29	2	I37303	HLA-DR beta - huma
704	2	6.7	29	2	I37306	HLA-DR beta - huma
705	2	6.7	29	2	I50214	protein-tyrosine-p
706	2	6.7	29	2	S07771	histone H2B.2, spe
707	2	6.7	29	2	T04412	histone H3 - barle
708	2	6.7	29	2	S51070	ribosomal protein
709	2	6.7	29	2	S08555	ribosomal protein
710	2	6.7	29	2	PC4231	ribosomal protein
711	2	6.7	29	2	S10050	ribosomal protein
712	2	6.7	29	2	S10049	ribosomal protein
713	2	6.7	29	2	S26229	ribosomal protein
714	2	6.7	29	2	A27561	Meth A tumor-speci
715	2	6.7	29	2	S10725	calmodulin-binding
716	2	6.7	29	2	E33208	calreticulin, uter
717	2	6.7	29	2	C33208	calreticulin, slow
718	2	6.7	29	2	D33208	calreticulin, brai
719	2	6.7	29	2	A45474	thrombospondin 2 -
720	2	6.7	29	2	G39690	neural cell adhesi
721	2	6.7	29	2	A61166	endometrial proges
722	2	6.7	29	2	I52402	alpha-fetoprotein
723	2	6.7	29	2	S57232	homeotic protein s
724	2	6.7	29	2	S06854	chorion class B pr
725	2	6.7	29	2	A43038	auxin-binding prot
726	2	6.7	29	2	T12082	proline-rich prote
727	2	6.7	29	2	S70328	gamma35 secalin -
728	2	6.7	29	2	S29208	avenin gamma-3 - o
729	2	6.7	29	2	S07055	photosystem I prot
730	2	6.7	29	2	S05032	photosystem II pro
731	2	6.7	29	2	S08088	gene VII protein -
732	2	6.7	29	2	F42075	finger protein (cl
733	2	6.7	29	2	T51116	probable precorrin
734	2	6.7	29	2	A53145	high conductance c
735	2	6.7	29	2	A35121	hypothetical prote
736	2	6.7	29	2	S03277	photosystem II 5K
737	2	6.7	29	2	A55891	delta-conotoxin Gm
738	2	6.7	29	2	S32730	homeotic protein -
739	2	6.7	29	2	S57225	labial protein (cl
740	2	6.7	29	2	S32732	homeotic protein -
741	2	6.7	29	2	S32734	homeotic protein -
742	2	6.7	29	2	S32733	homeotic protein -
743	2	6.7	29	2	G90719	hypothetical prote
744	2	6.7	29	2	S07513	gene 5.1 protein -
745	2	6.7	29	2	S14040	hypothetical prote
746	2	6.7	29	2	E64586	hypothetical prote
747	2	6.7	29	2	B64607	hypothetical prote
748	2	6.7	29	2	G64674	hypothetical prote
749	2	6.7	29	2	G83440	KdpF protein PA163
750	2	6.7	29	2	A49288	alcohol dehydrogen
751	2	6.7	29	2	A00774	3-oxoadipate enol-
752	2	6.7	29	2	A81078	hypothetical prote
753	2	6.7	29	2	B81006	hypothetical prote
754	2	6.7	29	2	T48910	KdpF protein [vali

755	2	6.7	29	2	A35445	repY protein - Esc
756	2	6.7	29	2	S19943	aadB protein - Kle
757	2	6.7	29	2	A49914	S-layer protein va
758	2	6.7	29	2	E64036	hypothetical prote
759	2	6.7	29	2	B48363	2-hydroxyglutaryl-
760	2	6.7	29	2	C40638	orf 3' of cycI - R
761	2	6.7	29	2	B56817	photosystem I chai
762	2	6.7	29	2	S74572	hypothetical prote
763	2	6.7	29	2	C60743	putrescine carbamo
764	2	6.7	29	2	S67989	HA-19/HA-52 protei
765	2	6.7	29	2	S14099	12-alpha-hydroxyst
766	2	6.7	29	2	S77569	plantaricin SA6 -
767	2	6.7	29	2	S21222	48K protein - Euba
768	2	6.7	29	2	S03947	hydrogen dehydroge
769	2	6.7	29	2	T37120	hypothetical prote
770	2	6.7	29	2	T36654	probable small mem
771	2	6.7	29	2	B43937	endo-1,4-beta-xyla
772	2	6.7	29	2	S09556	hypothetical prote
773	2	6.7	29	2	T06904	hypothetical prote
774	2	6.7	29	2	S73197	hypothetical prote
775	2	6.7	29	2	S78326	conserved hypothet
776	2	6.7	29	2	S78310	hypothetical prote
777	2	6.7	29	2	S78360	hypothetical prote
778	2	6.7	29	2	S01572	hypothetical prote
779	2	6.7	29	2	T07450	hypothetical prote
780	2	6.7	29	2	S01448	hypothetical prote
781	2	6.7	29	2	S38525	rRNA N-glycosidase
782	2	6.7	29	2	T52557	translation elonga
783	2	6.7	29	2	PQ0862	allantoinase (EC 3
784	2	6.7	29	2	PQ0486	globulin 2a - taro
785	2	6.7	29	2	S02200	prolamin alpha-1 -
786	2	6.7	29	2	A60683	malate dehydrogena
787	2	6.7	29	2	JQ0212	hypothetical 3K pr
788	2	6.7	29	2	S58541	hypothetical prote
789	2	6.7	29	2	PC2035	alanine transamina
790	2	6.7	29	2	S78714	protein YDR524w-a
791	2	6.7	29	2	B21112	variant surface gl
792	2	6.7	29	2	C60110	repetitive protein
793	2	6.7	29	2	D24802	cuticle protein 36
794	2	6.7	29	2	A56591	E75 steroid recept
795	2	6.7	29	2	A61613	ceratotoxin A - Me
796	2	6.7	29	2	B61613	ceratotoxin B - Me
797	2	6.7	29	2	PH1230	lectin - namazu (f
798	2	6.7	29	2	A32860	biotin-binding pro
799	2	6.7	29	2	I50382	c-mil protein - ch
800	2	6.7	29	2	I50695	non-collagenous al
801	2	6.7	29	2	B54197	70k thyroid autoan
802	2	6.7	29	2	A35891	carcinoembryonic a
803	2	6.7	29	2	I77372	CD44SP - human
804	2	6.7	29	2	S54340	diazepam binding i
805	2	6.7	29	2	A41683	hyaluronate recept
806	2	6.7	29	2	C54037	splicing regulator
807	2	6.7	29	2	S35924	T-cell receptor ga
808	2	6.7	29	2	C61384	trachael mucin gly
809	2	6.7	29	2	A60604	glutathione peroxi
810	2	6.7	29	2	S57204	oviduct-specific s
811	2	6.7	29	2	I47025	antigen WC1 [impor

812	2	6.7	29	2	A49410	t-complex polypept
813	2	6.7	29	2	PS0125	H-2 class I histoc
814	2	6.7	29	2	S46929	teg169 protein - m
815	2	6.7	29	2	S38749	vimentin homolog -
816	2	6.7	29	2	S42764	Ca2+/calmodulin-de
817	2	6.7	29	2	A49708	synaptosomal-assoc
818	2	6.7	29	2	H83777	hypothetical prote
819	2	6.7	29	2	C83833	hypothetical prote
820	2	6.7	29	2	F83870	hypothetical prote
821	2	6.7	29	2	B84144	hypothetical prote
822	2	6.7	29	2	PC4421	multactivase (EC 3
823	2	6.7	29	2	B85840	hypothetical prote
824	2	6.7	29	2	C85840	hypothetical prote
825	2	6.7	29	2	G86058	hypothetical prote
826	2	6.7	29	2	E89904	hypothetical prote
827	2	6.7	29	2	H89949	hypothetical prote
828	2	6.7	29	2	A59278	neurotoxin BmK A3-
829	2	6.7	29	2	S17496	inorganic diphosph
830	2	6.7	29	2	PQ0782	NADH2 dehydrogenas
831	2	6.7	29	2	S34762	L-serine ammonia-l
832	2	6.7	29	2	AB0717	hypothetical prote
833	2	6.7	29	2	AC0717	hypothetical prote
834	2	6.7	29	2	AH2338	PetN protein [limpo
835	2	6.7	29	4	I58970	hypothetical prote
836	2	6.7	30	1	AIBSAF	thermophilic amino
837	2	6.7	30	1	TIPU1W	trypsin inhibitor
838	2	6.7	30	1	OEON2K	beta-endorphin II
839	2	6.7	30	1	IRTRC3	protamine CIII, ma
840	2	6.7	30	1	IRTRC2	protamine Ia - rai
841	2	6.7	30	1	IRTR78	protamine CIII, mi
842	2	6.7	30	1	IRTR4	protamine PTP4 - r
843	2	6.7	30	1	CLHRY2	protamine YII - Pa
844	2	6.7	30	1	CLHR2A	protamine YII - At
845	2	6.7	30	1	SNUMP	sillucin - Rhizomu
846	2	6.7	30	2	I57689	ubiquinol-cytochro
847	2	6.7	30	2	I52254	gene CYP11B2 prote
848	2	6.7	30	2	B56859	fatty acid omega-h
849	2	6.7	30	2	A27375	photosystem I iron
850	2	6.7	30	2	S11131	NADH2 dehydrogenas
851	2	6.7	30	2	S14214	NADH2 dehydrogenas
852	2	6.7	30	2	S08202	peroxidase (EC 1.1
853	2	6.7	30	2	S08204	peroxidase (EC 1.1
854	2	6.7	30	2	S08203	peroxidase (EC 1.1
855	2	6.7	30	2	A39089	hydrogenase (EC 1.
856	2	6.7	30	2	I38066	nitric-oxide synth
857	2	6.7	30	2	I39799	CAT-66 - Bacillus
858	2	6.7	30	2	A18780	dimethylallyltrans
859	2	6.7	30	2	S03283	methionine adenosy
860	2	6.7	30	2	S71865	glutathione transf
861	2	6.7	30	2	B27103	aspartate transami
862	2	6.7	30	2	A27103	aspartate transami
863	2	6.7	30	2	I55427	aspartate transami
864	2	6.7	30	2	A49955	protein-tyrosine k
865	2	6.7	30	2	S68639	nigroxin A - black
866	2	6.7	30	2	S68640	nigroxin B - black
867	2	6.7	30	2	A05004	pancreatic ribonuc
868	2	6.7	30	2	D57001	endo-1,4-beta-xyla

869	2	6.7	30	2	A43937	endo-1,4-beta-xyla
870	2	6.7	30	2	PC2361	alpha-glucosidase
871	2	6.7	30	2	PX0073	epoxide hydrolase
872	2	6.7	30	2	B60291	30K serine protein
873	2	6.7	30	2	A27634	major fecal allerg
874	2	6.7	30	2	B27634	major fecal allerg
875	2	6.7	30	2	I77411	renin-2 - mouse (f
876	2	6.7	30	2	PC2328	proteasome endopep
877	2	6.7	30	2	A34486	inorganic diphosph
878	2	6.7	30	2	S21816	H+-exporting ATPas
879	2	6.7	30	2	S21814	H+-exporting ATPas
880	2	6.7	30	2	S74121	fructose-bisphosph
881	2	6.7	30	2	S25666	phosphopyruvate hy
882	2	6.7	30	2	S69600	peptidylprolyl iso
883	2	6.7	30	2	A60517	alpha-1-antitrypsi
884	2	6.7	30	2	S24979	proteinase inhibit
885	2	6.7	30	2	JX0057	trypsin inhibitor
886	2	6.7	30	2	JS0579	squash-type trypsi
887	2	6.7	30	2	JQ1958	trypsin inhibitor
888	2	6.7	30	2	PC1113	proteinase inhibit
889	2	6.7	30	2	C42842	antifungal 2S stor
890	2	6.7	30	2	S70341	napin large chain
891	2	6.7	30	2	S70343	napin large chain
892	2	6.7	30	2	A33308	thrombomodulin - r
893	2	6.7	30	2	S01657	atrial natriuretic
894	2	6.7	30	2	A61130	somatotropin - Ame
895	2	6.7	30	2	S44473	glucagon-like pept
896	2	6.7	30	2	A59076	defensin alpha-1 -
897	2	6.7	30	2	B59076	defensin alpha-2 -
898	2	6.7	30	2	C59076	defensin alpha-3 -
899	2	6.7	30	2	B60791	toxin II.6 - scorp
900	2	6.7	30	2	A31187	neurotoxin II.22.5
901	2	6.7	30	2	I68109	interferon alpha-W
902	2	6.7	30	2	C49533	T-cell receptor al
903	2	6.7	30	2	S20778	Ig heavy chain V r
904	2	6.7	30	2	PL0092	Ig heavy chain V r
905	2	6.7	30	2	PH0245	T-cell receptor Vb
906	2	6.7	30	2	PH0228	T-cell receptor Vb
907	2	6.7	30	2	PH0252	T-cell receptor Vb
908	2	6.7	30	2	PH0882	Ig kappa chain V r
909	2	6.7	30	2	E31461	T-cell receptor de
910	2	6.7	30	2	PH0235	T-cell receptor Vb
911	2	6.7	30	2	A49533	T-cell receptor al
912	2	6.7	30	2	C27579	T-cell receptor be
913	2	6.7	30	2	I37626	Fc gamma (IgG) rec
914	2	6.7	30	2	PS0121	H-2 class I histoc
915	2	6.7	30	2	S74192	crotoxin inhibitor
916	2	6.7	30	2	A05253	hemoglobin epsilon
917	2	6.7	30	2	A21680	hemoglobin epsilon
918	2	6.7	30	2	A05254	hemoglobin epsilon
919	2	6.7	30	2	S68618	histone H2B - sea
920	2	6.7	30	2	PD0014	cAMP response elem
921	2	6.7	30	2	S11613	ribosomal protein
922	2	6.7	30	2	S11617	ribosomal protein
923	2	6.7	30	2	A60511	gamma-crystallin -
924	2	6.7	30	2	I49412	gamma-crystallin-3
925	2	6.7	30	2	S12965	gamma-crystallin -

926	2	6.7	30	2	S69269	ezrin homolog - bo
927	2	6.7	30	2	A61189	tubulin beta chain
928	2	6.7	30	2	I52806	Duchenne muscular
929	2	6.7	30	2	S21153	calcium-binding pr
930	2	6.7	30	2	A26188	lipocortin I - pig
931	2	6.7	30	2	A56790	annexin, isoform P
932	2	6.7	30	2	A34622	fibrinogen beta ch
933	2	6.7	30	2	A03148	retinol-binding pr
934	2	6.7	30	2	A48299	taurine transporte
935	2	6.7	30	2	B61511	serum albumin, mil
936	2	6.7	30	2	B39819	neutrophil chemota
937	2	6.7	30	2	A38933	vitronectin - bovi
938	2	6.7	30	2	S57234	fushi tarazu segme
939	2	6.7	30	2	S69124	rRNA N-glycosidase
940	2	6.7	30	2	S69125	rRNA N-glycosidase
941	2	6.7	30	2	S07065	rRNA N-glycosidase
942	2	6.7	30	2	A31836	17K antigen - Rick
943	2	6.7	30	2	PQ0669	photosystem I 17.5
944	2	6.7	30	2	E45095	photosystem I ligh
945	2	6.7	30	2	B45095	photosystem I ligh
946	2	6.7	30	2	B24987	regulatory protein
947	2	6.7	30	2	S30757	genome polyprotein
948	2	6.7	30	2	S30760	genome polyprotein
949	2	6.7	30	2	S30759	genome polyprotein
950	2	6.7	30	2	B44314	intracisternal A p
951	2	6.7	30	2	S26175	tail tubular prote
952	2	6.7	30	2	S69352	N-methylhydantoin
953	2	6.7	30	2	S68312	glucuronosyltransf
954	2	6.7	30	2	S42364	aromatic-amino-aci
955	2	6.7	30	2	S05223	photosystem I 6.5K
956	2	6.7	30	2	S28991	antifungal protein
957	2	6.7	30	2	PC2307	X-Pro aminopeptida
958	2	6.7	30	2	PQ0484	globulin 1b - taro
959	2	6.7	30	2	C43591	51K outer membrane
960	2	6.7	30	2	B43591	45K outer membrane
961	2	6.7	30	2	S06411	killer plasmid 28K
962	2	6.7	30	2	B49292	GDP dissociation i
963	2	6.7	30	2	A60914	pheromone-binding
964	2	6.7	30	2	PS0437	potassium channel
965	2	6.7	30	2	PS0438	potassium channel
966	2	6.7	30	2	A47607	immunogenic protei
967	2	6.7	30	2	S02088	blood group Rh-rel
968	2	6.7	30	2	S29138	aniline monooxygen
969	2	6.7	30	2	S57227	proboscipedia prot
970	2	6.7	30	2	B95020	hypothetical prote
971	2	6.7	30	2	C95030	hypothetical prote
972	2	6.7	30	2	G95031	hypothetical prote
973	2	6.7	30	2	E95079	hypothetical prote
974	2	6.7	30	2	F95118	hypothetical prote
975	2	6.7	30	2	E95145	hypothetical prote
976	2	6.7	30	2	F89406	protein R10E8.7 [i
977	2	6.7	30	2	F87254	hypothetical prote
978	2	6.7	30	2	E84786	hypothetical prote
979	2	6.7	30	2	C84481	hypothetical prote
980	2	6.7	30	2	B47483	cysteine-rich para
981	2	6.7	30	2	S15141	hypothetical prote
982	2	6.7	30	2	S13985	hypothetical prote

983	2	6.7	30	2	S14038	hypothetical prote
984	2	6.7	30	2	S13994	hypothetical prote
985	2	6.7	30	2	A72205	hypothetical prote
986	2	6.7	30	2	E72356	hypothetical prote
987	2	6.7	30	2	H72312	hypothetical prote
988	2	6.7	30	2	S66448	trimethylamine deh
989	2	6.7	30	2	A70105	conserved hypothet
990	2	6.7	30	2	F70118	hypothetical prote
991	2	6.7	30	2	D70144	hypothetical prote
992	2	6.7	30	2	H70152	hypothetical prote
993	2	6.7	30	2	A70209	hypothetical prote
994	2	6.7	30	2	E70246	hypothetical prote
995	2	6.7	30	2	F70253	hypothetical prote
996	2	6.7	30	2	F70254	hypothetical prote
997	2	6.7	30	2	H64522	hypothetical prote
998	2	6.7	30	2	E64565	hypothetical prote
999	2	6.7	30	2	E64577	hypothetical prote
1000	2	6.7	30	2	C64709	hypothetical prote

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 16.7%; Score 5; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28

||||

Db 26 LRKKL 30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 16.7%; Score 5; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5

|||||

Db 30 SVSEI 34

RESULT 3

E95098

hypothetical protein SP0853 [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:
A;Gene: SP0853

Query Match 16.7%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 4

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.

submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity
homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 13.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 5

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: A55527

R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;

Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.

J. Bacteriol. 176, 1746-1755, 1994

A;Title: Isolation, phenotypic characterization, and complementation analysis of
mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline
quinone and sequences of pqqD, pqqG, and pqqC.

A;Reference number: A55527; MUID:94179111; PMID:8132470

A;Accession: A55527

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-29 <MOR>
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
C;Genetics:
A;Gene: pqqD
C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 13.3%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 8 VSEI 11

RESULT 6

S01614
dystrophin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S01614
R;Nudel, U.; Robzyk, K.; Yaffe, D.
Nature 331, 635-638, 1988
A;Title: Expression of the putative Duchenne muscular dystrophy gene in differentiated myogenic cell cultures and in the brain.
A;Reference number: S01614; MUID:88122671; PMID:3340214
A;Accession: S01614
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <NUD>
A;Cross-references: EMBL:X07000; NID:g56137; PIDN:CAA30057.1; PID:g1334214
C;Genetics:
A;Map position: X
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat homology; WW repeat homology
C;Keywords: actin binding; cytoskeleton

Query Match 13.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 7

I78537
copper transporting P-type ATPase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I78537
R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.

Nature Genet. 9, 210-217, 1995
A;Title: The Wilson disease gene: spectrum of mutations and their consequences.
A;Reference number: I58128; MUID:95235569; PMID:7626145
A;Accession: I78537
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-29 <RES>
A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355
C;Genetics:
A;Gene: GDB:ATP7B
A;Cross-references: GDB:120494; OMIM:277900
A;Map position: 13q14.3-13q21.1

Query Match 13.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
|||
Db 14 SEIQ 17

RESULT 8

S78412
ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78412; S78413
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78412
A;Molecule type: protein
A;Residues: 1-29 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein L22
A;Accession: S78413
A;Molecule type: protein
A;Residues: 1-10,'XXP',14-15,'X',17-24 <GO2>
A;Note: the protein is designated as mitochondrial ribosomal protein L24
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 13.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 4 LRKK 7

RESULT 9

S63531
hypothetical protein 1 - Sulfolobus solfataricus (fragment)
C;Species: Sulfolobus solfataricus
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.
 Eur. J. Biochem. 233, 800-808, 1995
 A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate
 dehydrogenase genes from the thermophilic archaeon *Sulfolobus solfataricus*
 overlap by 8-bp: isolation, sequencing of the genes and expression in
Escherichia coli.
 A;Reference number: S63528; MUID:96085144; PMID:8521845
 A;Accession: S63531
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-30 <JON>
 A;Cross-references: EMBL:X80178

Query Match 13.3%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
 Db 11 WLRK 14

RESULT 10

S44471
 glucagon G1 - North American paddlefish (*Polyodon spathula*)
 C;Species: *Polyodon spathula*
 C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999
 C;Accession: S44471
 R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
 Biochem. J. 300, 339-345, 1994
 A;Title: Characterization of insulins and proglucagon-derived peptides from a
 phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).
 A;Reference number: S44467; MUID:94271144; PMID:8002937
 A;Accession: S44471
 A;Molecule type: protein
 A;Residues: 1-31 <NGU>
 A;Experimental source: pancreas
 C;Superfamily: glucagon
 C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas
 F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 13.3%; Score 4; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
 ||||
 Db 23 VEWL 26

RESULT 11

S44472
 glucagon G2 - North American paddlefish (*Polyodon spathula*)
 C;Species: *Polyodon spathula*
 C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999
 C;Accession: S44472
 R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 13.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
 ||||
Db 23 VEWL 26

RESULT 12

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058; TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 13.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 26 KKLQ 29

RESULT 13

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 13.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 26 SVSE 29

RESULT 14

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 13.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
|||
Db 8 MERV 11

RESULT 15

G84161

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84161
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: G84161
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-32 <STO>
 A;Cross-references: GB:AE004437; NID:g10579667; PIDN:AAG18659.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: VNG0019H

Query Match 13.3%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
 ||||
 Db 13 KLQD 16

RESULT 16

E81714
 hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
 C;Accession: E81714
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser, C.M.
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: E81714
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-33 <TET>
 A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1; PID:g7190379; GSPDB:GN00121; TIGR:TC0337
 A;Experimental source: strain Nigg (MoPn)
 C;Genetics:
 A;Gene: TC0337

Query Match 13.3%; Score 4; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
Db 26 LRKK 29

RESULT 17

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 13.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
 ||||
Db 29 SVSE 32

RESULT 18

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 13.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
 ||||
Db 29 SVSE 32

RESULT 19

D82125

hypothetical protein VC2034 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82125

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82125

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <HEI>

A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1; GSPDB:GN00126; TIGR:VC2034

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2034

A;Map position: 1

Query Match 13.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 24 KKLQ 27

RESULT 20

S70806

hypothetical protein 5 - *Vibrio cholerae* (fragment)

N;Alternate names: flagellar protein flaA homolog

C;Species: *Vibrio cholerae*

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-Aug-1999

C;Accession: S70806

R;Camilli, A.; Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A;Title: Use of recombinase gene fusions to identify *Vibrio cholerae* genes induced during infection.

A;Reference number: S70798; MUID:96414469; PMID:8817490

A;Accession: S70806

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-36 <CAM>

A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196

C;Superfamily: flagellin

Query Match 13.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20

||||

Db 14 SMER 17

RESULT 21

F95057

hypothetical protein SP0497 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: F95057

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95057

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164; TIGR:SP4SP0497

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0497

Query Match 13.3%; Score 4; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29

||||

Db 10 KKLQ 13

RESULT 22

A84774

hypothetical protein At2g35870 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84774

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g35870

A;Map position: 2

Query Match 13.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29

||||

Db 4 KKLQ 7

RESULT 23

S46227

hypothetical protein - *Streptomyces chrysomallus* (fragment)

C;Species: *Streptomyces chrysomallus*

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: *Streptomyces chrysomallus* FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 13.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22

||||

Db 27 ERVE 30

RESULT 24

S71912

hemoglobin, extracellular, chain A1 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71912

A;Molecule type: protein

A;Residues: 1-37 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 13.3%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22

||||

Db 25 ERVE 28

RESULT 25

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: *Helianthus annuus* (common sunflower)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169

A;Accession: T12635

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259

C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 13.3%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28

||||

Db 6 RKKL 9

RESULT 26

CKFHCS

sarcotoxin IC - flesh fly (*Sarcophaga peregrina*)

C;Species: *Sarcophaga peregrina*

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997
A;Accession: C22625
A;Molecule type: protein
A;Residues: 1-39 <OKA>
C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.
C;Superfamily: cecropin
C;Keywords: amidated carboxyl end; antibacterial; hemolymph
F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 13.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 2 WLRK 5

RESULT 27

S71913

hemoglobin, extracellular, chain A2 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71913

A;Molecule type: protein

A;Residues: 1-39 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 13.3%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 28

A42272

brain-type creatine kinase, peptide B - spiny dogfish (fragment)

C;Species: *Squalus acanthias* (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium chloride transporting epithelia of the spiny dogfish, *Squalus acanthias*.
A;Reference number: A42272; MUID:92156175; PMID:1310991
A;Accession: A42272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <FRI>
A;Note: sequence extracted from NCBI backbone (NCBIP:82919)
C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 10 KKL 12

RESULT 29

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake (fragment)

C;Species: *Pseudechis porphyriacus* (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin phospholipases A-2 from *Pseudechis porphyriacus* (Australian red-bellied black snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
|||
Db 3 IQL 5

RESULT 30

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: *Macaca mulatta* (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 31

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.

A;Reference number: A60304

A;Accession: A60304

A;Molecule type: protein

A;Residues: 1-28 <ENG>

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 32

S58386

T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999

C;Accession: S58386

R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.

Nucleic Acids Res. 23, 3074-3075, 1995

A;Title: A novel method for sequencing members of multi-gene families.

A;Reference number: S58384; MUID:95388532; PMID:7659534

A;Accession: S58386

A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-28 <JOH>
A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
A;Note: only a part of the coding sequence is given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
|||
Db 12 ERV 14

RESULT 33

PN0047

signal transduction protein QM0017 - mouse (fragments)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 15-Oct-1999

C;Accession: PN0047

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0047

A;Molecule type: protein

A;Residues: 1-28 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 25,600 and the pI is 6.07. The amino-terminus is blocked.

C;Superfamily: signal transduction protein DJ-1

C;Keywords: brain

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 14 NLG 16

RESULT 34

S70894

hypothetical protein 1 - Vibrio anguillarum (fragment)

C;Species: Vibrio anguillarum

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S70894

R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.

Mol. Microbiol. 19, 625-637, 1996

A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen *Vibrio anguillarum*.

A;Reference number: S70894; MUID:96228710; PMID:8830252

A;Accession: S70894

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <OTO>

A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1; PID:g1723992

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 35

S22469

hypothetical protein 1 - *Prochlorothrix hollandica*

C;Species: *Prochlorothrix hollandica*

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C;Accession: S22469; S16850

R;Greer, K.L.; Golden, S.S.

Plant Mol. Biol. 19, 355-365, 1992

A;Title: Conserved relationship between psbH and petBD genes: presence of a shared upstream element in *Prochlorothrix hollandica*.

A;Reference number: S22469; MUID:92322967; PMID:1623188

A;Accession: S22469

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <GRE>

A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3
|||
Db 4 SVS 6

RESULT 36

S26254

rel protein - chicken

C;Species: *Gallus gallus* (chicken)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Dec-1996

C;Accession: S26254

R;Capobianco, A.J.; Gilmore, T.D.

Oncogene 6, 2203-2210, 1991

A;Title: Repression of the chicken c-rel promoter by vRel in chicken embryo fibroblasts is not mediated through a consensus NF-kappaB binding site.

A;Reference number: S26254; MUID:92115319; PMID:1766669

A;Accession: S26254

A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <CAP>
A;Cross-references: EMBL:X59588

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RVE 22
|||
Db 1 RVE 3

RESULT 37

I59477

antigen, T-cell receptor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000

C;Accession: I59477

R;Mathioudakis, G.; Chen, P.

Scand. J. Immunol. 38, 31-36, 1993

A;Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the T-cell antigen receptor to J gamma 2C gamma 2 gene segments in peripheral blood lymphocyte transcripts from normal donors.

A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:g181658

C;Keywords: T-cell receptor

Query Match 10.0%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 10 KKL 12

RESULT 38

F46522

T-cell receptor eta chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: F46522; I56191

R;Jensen, J.P.; Cenciarelli, C.; Hou, D.; Rellahan, B.L.; Dean, M.; Weissman, A.M.

J. Immunol. 150, 122-130, 1993

A;Title: T cell antigen receptor-eta subunit. Low levels of expression and limited cross-species conservation.

A;Reference number: A46522; MUID:93107707; PMID:8417118

A;Accession: F46522

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-28 <JEN>
 A;Cross-references: GB:S51404; NID:g262180; PIDN:AAB24606.1; PID:g262181
 A;Note: sequence extracted from NCBI backbone (NCBIP:120909)
 R;Itoh, Y.; Matsuura, A.; Kinebuchi, M.; Honda, R.; Takayama, S.; Ichimiya, S.;
 Kon, S.; Kikuchi, K.
 J. Immunol. 151, 4705-4717, 1993
 A;Title: Structural analysis of the CD3 zeta/eta locus of the rat. Expression of
 zeta but eta transcripts by rat T cells.
 A;Reference number: I56191; MUID:94014415; PMID:8409430
 A;Accession: I56191
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-28 <RES>
 A;Cross-references: GB:D13556; NID:g436580; PIDN:BAA02754.1; PID:g436581
 C;Keywords: T-cell receptor

Query Match 10.0%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
 |||
 Db 13 RKK 15

RESULT 39

H85908

hypothetical protein Z3917 [imported] - Escherichia coli (strain O157:H7,
 substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: H85908

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
 D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.;
 Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis,
 N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca, J.; Anantharaman, T.S.;
 Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
 Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: H85908

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <STO>

A;Cross-references: GB:AE005174; NID:g12517049; PIDN:AAG57732.1; GSPDB:GN00145;
 UWGP:Z3917

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z3917

Query Match 10.0%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30
 |||
 Db 9 LQD 11

RESULT 40

GCCB

glucagon - Chinchilla brevicaudata

C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998

C;Accession: A60413

R;Eng, J.; Kleinman, W.A.; Chu, L.S.

Peptides 11, 683-685, 1990

A;Title: Purification of peptide hormones from chinchilla pancreas by chemical assay.

A;Reference number: A60413; MUID:91045327; PMID:2235678

A;Accession: A60413

A;Molecule type: protein

A;Residues: 1-29 <ENG>

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

Query Match 10.0%; Score 3; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15

|||

Db 12 KHL 14

Search completed: January 14, 2004, 10:37:27

Job time : 9.8785 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 20.1869 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-166
Perfect score: 30
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	30	100.0	30	11	US-09-843-221A-39	Sequence 39, Appl
2	30	100.0	30	11	US-09-843-221A-166	Sequence 166, App
3	30	100.0	31	9	US-09-169-786-2	Sequence 2, Appli
4	30	100.0	31	11	US-09-843-221A-27	Sequence 27, Appl
5	30	100.0	31	11	US-09-843-221A-165	Sequence 165, App
6	30	100.0	33	12	US-10-361-928-9	Sequence 9, Appli
7	30	100.0	34	9	US-09-169-786-3	Sequence 3, Appli
8	30	100.0	34	10	US-09-928-047B-6	Sequence 6, Appli
9	30	100.0	34	11	US-09-843-221A-16	Sequence 16, Appl
10	30	100.0	34	11	US-09-843-221A-161	Sequence 161, App
11	30	100.0	34	12	US-09-928-048A-6	Sequence 6, Appli
12	30	100.0	34	12	US-10-361-928-8	Sequence 8, Appli
13	30	100.0	34	12	US-10-340-484-15	Sequence 15, Appl
14	30	100.0	34	12	US-10-340-484-16	Sequence 16, Appl
15	30	100.0	34	14	US-10-016-403-5	Sequence 5, Appli
16	30	100.0	34	14	US-10-097-079-1	Sequence 1, Appli
17	30	100.0	37	12	US-10-168-185-9	Sequence 9, Appli
18	30	100.0	38	9	US-09-169-786-4	Sequence 4, Appli
19	30	100.0	38	11	US-09-843-221A-14	Sequence 14, Appl
20	30	100.0	38	12	US-10-245-707-1	Sequence 1, Appli
21	29	96.7	29	11	US-09-843-221A-51	Sequence 51, Appl
22	29	96.7	29	11	US-09-843-221A-167	Sequence 167, App
23	29	96.7	30	11	US-09-843-221A-43	Sequence 43, Appl
24	29	96.7	33	12	US-10-361-928-3	Sequence 3, Appli
25	29	96.7	33	12	US-10-361-928-6	Sequence 6, Appli
26	29	96.7	34	11	US-09-843-221A-20	Sequence 20, Appl
27	29	96.7	34	12	US-10-361-928-1	Sequence 1, Appli
28	29	96.7	34	12	US-10-361-928-2	Sequence 2, Appli
29	29	96.7	34	12	US-10-361-928-5	Sequence 5, Appli
30	29	96.7	37	11	US-09-843-221A-15	Sequence 15, Appl
31	28	93.3	28	11	US-09-843-221A-52	Sequence 52, Appl
32	28	93.3	28	11	US-09-843-221A-168	Sequence 168, App
33	28	93.3	34	14	US-10-016-403-7	Sequence 7, Appli
34	27	90.0	34	12	US-10-372-095-24	Sequence 24, Appl
35	26	86.7	30	11	US-09-843-221A-50	Sequence 50, Appl
36	26	86.7	31	11	US-09-843-221A-28	Sequence 28, Appl
37	26	86.7	31	12	US-10-031-874A-206	Sequence 206, App
38	24	80.0	28	11	US-09-843-221A-32	Sequence 32, Appl
39	24	80.0	34	14	US-10-016-403-6	Sequence 6, Appli
40	22	73.3	30	11	US-09-843-221A-124	Sequence 124, App
41	22	73.3	30	11	US-09-843-221A-125	Sequence 125, App
42	22	73.3	34	11	US-09-843-221A-88	Sequence 88, Appl
43	22	73.3	34	11	US-09-843-221A-89	Sequence 89, Appl
44	21	70.0	30	11	US-09-843-221A-126	Sequence 126, App
45	21	70.0	30	11	US-09-843-221A-127	Sequence 127, App
46	21	70.0	34	11	US-09-843-221A-90	Sequence 90, Appl
47	21	70.0	34	11	US-09-843-221A-91	Sequence 91, Appl
48	21	70.0	34	11	US-09-843-221A-92	Sequence 92, Appl
49	21	70.0	34	11	US-09-843-221A-128	Sequence 128, App
50	19	63.3	30	11	US-09-843-221A-40	Sequence 40, Appl
51	19	63.3	30	11	US-09-843-221A-41	Sequence 41, Appl
52	19	63.3	34	11	US-09-843-221A-17	Sequence 17, Appl
53	19	63.3	34	11	US-09-843-221A-18	Sequence 18, Appl
54	19	63.3	34	11	US-09-843-221A-162	Sequence 162, App
55	19	63.3	34	11	US-09-843-221A-163	Sequence 163, App
56	18	60.0	30	11	US-09-843-221A-42	Sequence 42, Appl

57	18	60.0	34	11	US-09-843-221A-19	Sequence 19, Appl
58	18	60.0	34	11	US-09-843-221A-164	Sequence 164, App
59	17	56.7	34	12	US-10-340-484-17	Sequence 17, Appl
60	16	53.3	28	11	US-09-843-221A-93	Sequence 93, Appl
61	16	53.3	28	11	US-09-843-221A-94	Sequence 94, Appl
62	15	50.0	28	11	US-09-843-221A-95	Sequence 95, Appl
63	15	50.0	28	11	US-09-843-221A-96	Sequence 96, Appl
64	15	50.0	28	11	US-09-843-221A-97	Sequence 97, Appl
65	15	50.0	30	11	US-09-843-221A-47	Sequence 47, Appl
66	15	50.0	34	11	US-09-843-221A-24	Sequence 24, Appl
67	15	50.0	34	12	US-10-340-484-19	Sequence 19, Appl
68	14	46.7	28	11	US-09-843-221A-34	Sequence 34, Appl
69	14	46.7	28	11	US-09-843-221A-35	Sequence 35, Appl
70	14	46.7	28	11	US-09-843-221A-54	Sequence 54, Appl
71	14	46.7	30	11	US-09-843-221A-45	Sequence 45, Appl
72	14	46.7	30	11	US-09-843-221A-48	Sequence 48, Appl
73	14	46.7	32	11	US-09-843-221A-30	Sequence 30, Appl
74	14	46.7	34	11	US-09-843-221A-22	Sequence 22, Appl
75	14	46.7	34	11	US-09-843-221A-25	Sequence 25, Appl
76	14	46.7	34	12	US-10-340-484-18	Sequence 18, Appl
77	14	46.7	34	12	US-10-340-484-20	Sequence 20, Appl
78	14	46.7	34	12	US-10-340-484-22	Sequence 22, Appl
79	14	46.7	34	12	US-10-340-484-23	Sequence 23, Appl
80	14	46.7	40	15	US-10-014-162-111	Sequence 111, App
81	12	40.0	28	11	US-09-843-221A-33	Sequence 33, Appl
82	12	40.0	28	11	US-09-843-221A-36	Sequence 36, Appl
83	12	40.0	28	11	US-09-843-221A-53	Sequence 53, Appl
84	12	40.0	28	11	US-09-843-221A-55	Sequence 55, Appl
85	12	40.0	30	11	US-09-843-221A-44	Sequence 44, Appl
86	12	40.0	30	11	US-09-843-221A-46	Sequence 46, Appl
87	12	40.0	32	11	US-09-843-221A-29	Sequence 29, Appl
88	12	40.0	32	11	US-09-843-221A-31	Sequence 31, Appl
89	12	40.0	34	9	US-09-169-786-11	Sequence 11, Appl
90	12	40.0	34	11	US-09-843-221A-21	Sequence 21, Appl
91	12	40.0	34	11	US-09-843-221A-23	Sequence 23, Appl
92	10	33.3	31	9	US-09-169-786-9	Sequence 9, Appli
93	9	30.0	28	14	US-10-097-079-54	Sequence 54, Appl
94	9	30.0	28	14	US-10-097-079-62	Sequence 62, Appl
95	9	30.0	28	14	US-10-097-079-65	Sequence 65, Appl
96	9	30.0	28	14	US-10-097-079-79	Sequence 79, Appl
97	9	30.0	29	14	US-10-097-079-53	Sequence 53, Appl
98	9	30.0	29	14	US-10-097-079-63	Sequence 63, Appl
99	9	30.0	30	14	US-10-097-079-52	Sequence 52, Appl
100	9	30.0	30	14	US-10-097-079-64	Sequence 64, Appl
101	9	30.0	31	14	US-10-097-079-3	Sequence 3, Appli
102	9	30.0	31	14	US-10-097-079-4	Sequence 4, Appli
103	9	30.0	31	14	US-10-097-079-5	Sequence 5, Appli
104	9	30.0	31	14	US-10-097-079-6	Sequence 6, Appli
105	9	30.0	31	14	US-10-097-079-7	Sequence 7, Appli
106	9	30.0	31	14	US-10-097-079-8	Sequence 8, Appli
107	9	30.0	31	14	US-10-097-079-9	Sequence 9, Appli
108	9	30.0	31	14	US-10-097-079-10	Sequence 10, Appl
109	9	30.0	31	14	US-10-097-079-20	Sequence 20, Appl
110	9	30.0	31	14	US-10-097-079-21	Sequence 21, Appl
111	9	30.0	31	14	US-10-097-079-22	Sequence 22, Appl
112	9	30.0	31	14	US-10-097-079-23	Sequence 23, Appl
113	9	30.0	31	14	US-10-097-079-24	Sequence 24, Appl

114	9	30.0	31	14	US-10-097-079-25	Sequence 25, Appl
115	9	30.0	31	14	US-10-097-079-26	Sequence 26, Appl
116	9	30.0	31	14	US-10-097-079-27	Sequence 27, Appl
117	9	30.0	31	14	US-10-097-079-36	Sequence 36, Appl
118	9	30.0	31	14	US-10-097-079-37	Sequence 37, Appl
119	9	30.0	31	14	US-10-097-079-38	Sequence 38, Appl
120	9	30.0	31	14	US-10-097-079-39	Sequence 39, Appl
121	9	30.0	31	14	US-10-097-079-47	Sequence 47, Appl
122	9	30.0	31	14	US-10-097-079-48	Sequence 48, Appl
123	9	30.0	31	14	US-10-097-079-49	Sequence 49, Appl
124	9	30.0	31	14	US-10-097-079-50	Sequence 50, Appl
125	9	30.0	31	14	US-10-097-079-51	Sequence 51, Appl
126	9	30.0	31	14	US-10-097-079-69	Sequence 69, Appl
127	9	30.0	31	14	US-10-097-079-70	Sequence 70, Appl
128	9	30.0	31	14	US-10-097-079-74	Sequence 74, Appl
129	9	30.0	31	14	US-10-097-079-81	Sequence 81, Appl
130	9	30.0	31	14	US-10-097-079-82	Sequence 82, Appl
131	9	30.0	31	14	US-10-097-079-83	Sequence 83, Appl
132	9	30.0	31	14	US-10-097-079-84	Sequence 84, Appl
133	9	30.0	31	14	US-10-097-079-85	Sequence 85, Appl
134	9	30.0	34	14	US-10-097-079-46	Sequence 46, Appl
135	8	26.7	28	14	US-10-097-079-78	Sequence 78, Appl
136	8	26.7	30	11	US-09-843-221A-49	Sequence 49, Appl
137	8	26.7	30	11	US-09-843-221A-158	Sequence 158, App
138	8	26.7	30	11	US-09-843-221A-159	Sequence 159, App
139	8	26.7	31	9	US-09-169-786-10	Sequence 10, Appl
140	8	26.7	31	14	US-10-097-079-11	Sequence 11, Appl
141	8	26.7	31	14	US-10-097-079-19	Sequence 19, Appl
142	8	26.7	31	14	US-10-097-079-28	Sequence 28, Appl
143	8	26.7	31	14	US-10-097-079-35	Sequence 35, Appl
144	8	26.7	31	14	US-10-097-079-40	Sequence 40, Appl
145	8	26.7	31	14	US-10-097-079-45	Sequence 45, Appl
146	8	26.7	31	14	US-10-097-079-66	Sequence 66, Appl
147	8	26.7	31	14	US-10-097-079-67	Sequence 67, Appl
148	8	26.7	31	14	US-10-097-079-68	Sequence 68, Appl
149	8	26.7	31	14	US-10-097-079-73	Sequence 73, Appl
150	8	26.7	31	14	US-10-097-079-76	Sequence 76, Appl
151	8	26.7	31	14	US-10-097-079-80	Sequence 80, Appl
152	8	26.7	34	11	US-09-843-221A-26	Sequence 26, Appl
153	8	26.7	34	11	US-09-843-221A-122	Sequence 122, App
154	8	26.7	34	11	US-09-843-221A-123	Sequence 123, App
155	8	26.7	34	12	US-10-372-095-22	Sequence 22, Appl
156	8	26.7	34	14	US-10-097-079-75	Sequence 75, Appl
157	7	23.3	31	14	US-10-097-079-12	Sequence 12, Appl
158	7	23.3	31	14	US-10-097-079-18	Sequence 18, Appl
159	7	23.3	31	14	US-10-097-079-29	Sequence 29, Appl
160	7	23.3	31	14	US-10-097-079-34	Sequence 34, Appl
161	7	23.3	31	14	US-10-097-079-41	Sequence 41, Appl
162	7	23.3	31	14	US-10-097-079-44	Sequence 44, Appl
163	7	23.3	34	12	US-10-340-484-24	Sequence 24, Appl
164	6	20.0	30	11	US-09-843-221A-77	Sequence 77, Appl
165	6	20.0	31	14	US-10-097-079-13	Sequence 13, Appl
166	6	20.0	31	14	US-10-097-079-14	Sequence 14, Appl
167	6	20.0	31	14	US-10-097-079-15	Sequence 15, Appl
168	6	20.0	31	14	US-10-097-079-16	Sequence 16, Appl
169	6	20.0	31	14	US-10-097-079-17	Sequence 17, Appl
170	6	20.0	31	14	US-10-097-079-30	Sequence 30, Appl

171	6	20.0	31	14	US-10-097-079-31	Sequence 31, Appl
172	6	20.0	31	14	US-10-097-079-32	Sequence 32, Appl
173	6	20.0	31	14	US-10-097-079-33	Sequence 33, Appl
174	6	20.0	31	14	US-10-097-079-42	Sequence 42, Appl
175	6	20.0	31	14	US-10-097-079-43	Sequence 43, Appl
176	6	20.0	31	14	US-10-097-079-86	Sequence 86, Appl
177	6	20.0	31	14	US-10-097-079-87	Sequence 87, Appl
178	6	20.0	31	14	US-10-097-079-88	Sequence 88, Appl
179	6	20.0	36	11	US-09-843-221A-65	Sequence 65, Appl
180	5	16.7	28	11	US-09-843-221A-69	Sequence 69, Appl
181	5	16.7	28	11	US-09-843-221A-169	Sequence 169, App
182	5	16.7	34	9	US-09-864-761-38558	Sequence 38558, A
183	5	16.7	34	12	US-10-317-832-178	Sequence 178, App
184	5	16.7	38	9	US-09-864-761-49110	Sequence 49110, A
185	4	13.3	28	9	US-09-864-761-37690	Sequence 37690, A
186	4	13.3	28	9	US-09-929-818-122	Sequence 122, App
187	4	13.3	28	9	US-09-929-818-200	Sequence 200, App
188	4	13.3	28	10	US-09-003-869-153	Sequence 153, App
189	4	13.3	28	10	US-09-999-745-38	Sequence 38, Appl
190	4	13.3	28	10	US-09-554-000-22	Sequence 22, Appl
191	4	13.3	28	11	US-09-756-690A-153	Sequence 153, App
192	4	13.3	28	11	US-09-776-724A-198	Sequence 198, App
193	4	13.3	28	11	US-09-899-495-104	Sequence 104, App
194	4	13.3	28	12	US-10-029-386-28289	Sequence 28289, A
195	4	13.3	28	15	US-10-157-224A-153	Sequence 153, App
196	4	13.3	28	15	US-10-187-051-153	Sequence 153, App
197	4	13.3	29	9	US-09-730-379B-5	Sequence 5, Appli
198	4	13.3	29	11	US-09-983-802-386	Sequence 386, App
199	4	13.3	29	11	US-09-983-802-480	Sequence 480, App
200	4	13.3	29	11	US-09-969-730-133	Sequence 133, App
201	4	13.3	29	11	US-09-095-478-24	Sequence 24, Appl
202	4	13.3	29	12	US-09-933-767-1006	Sequence 1006, Ap
203	4	13.3	29	15	US-10-023-282-1006	Sequence 1006, Ap
204	4	13.3	29	15	US-10-106-698-5404	Sequence 5404, Ap
205	4	13.3	29	15	US-10-197-954-111	Sequence 111, App
206	4	13.3	30	9	US-09-864-761-41441	Sequence 41441, A
207	4	13.3	30	9	US-09-864-761-46868	Sequence 46868, A
208	4	13.3	30	10	US-09-756-983-20	Sequence 20, Appl
209	4	13.3	30	11	US-09-774-639-191	Sequence 191, App
210	4	13.3	30	12	US-09-911-261A-20	Sequence 20, Appl
211	4	13.3	30	12	US-10-310-113-19	Sequence 19, Appl
212	4	13.3	30	12	US-09-933-767-821	Sequence 821, App
213	4	13.3	30	12	US-10-173-551-40	Sequence 40, Appl
214	4	13.3	30	15	US-10-188-947-11	Sequence 11, Appl
215	4	13.3	30	15	US-10-057-408-20	Sequence 20, Appl
216	4	13.3	30	15	US-10-023-282-821	Sequence 821, App
217	4	13.3	31	9	US-09-864-761-38725	Sequence 38725, A
218	4	13.3	31	9	US-09-864-761-40464	Sequence 40464, A
219	4	13.3	31	9	US-09-864-761-44182	Sequence 44182, A
220	4	13.3	31	10	US-09-738-626-6281	Sequence 6281, Ap
221	4	13.3	31	12	US-10-360-053-20	Sequence 20, Appl
222	4	13.3	31	12	US-09-933-767-1001	Sequence 1001, Ap
223	4	13.3	31	12	US-10-029-386-32285	Sequence 32285, A
224	4	13.3	31	12	US-10-264-049-3767	Sequence 3767, Ap
225	4	13.3	31	15	US-10-023-282-1001	Sequence 1001, Ap
226	4	13.3	31	15	US-10-106-698-7956	Sequence 7956, Ap
227	4	13.3	32	9	US-09-864-761-48632	Sequence 48632, A

228	4	13.3	32	9	US-09-281-717-16	Sequence 16, Appl
229	4	13.3	32	11	US-09-809-391-442	Sequence 442, App
230	4	13.3	32	12	US-09-882-171-442	Sequence 442, App
231	4	13.3	32	12	US-10-310-113-23	Sequence 23, Appl
232	4	13.3	32	12	US-10-310-113-134	Sequence 134, App
233	4	13.3	32	12	US-10-310-113-135	Sequence 135, App
234	4	13.3	32	12	US-10-310-113-136	Sequence 136, App
235	4	13.3	32	12	US-10-164-279-39	Sequence 39, Appl
236	4	13.3	32	12	US-10-164-279-43	Sequence 43, Appl
237	4	13.3	32	15	US-10-174-410-212	Sequence 212, App
238	4	13.3	33	9	US-09-864-761-35714	Sequence 35714, A
239	4	13.3	33	9	US-09-864-761-48253	Sequence 48253, A
240	4	13.3	33	9	US-09-864-761-49019	Sequence 49019, A
241	4	13.3	33	9	US-09-925-299-1526	Sequence 1526, Ap
242	4	13.3	33	11	US-09-925-299-1526	Sequence 1526, Ap
243	4	13.3	33	11	US-09-809-391-660	Sequence 660, App
244	4	13.3	33	12	US-09-882-171-660	Sequence 660, App
245	4	13.3	33	12	US-09-933-767-368	Sequence 368, App
246	4	13.3	33	12	US-10-164-279-63	Sequence 63, Appl
247	4	13.3	33	14	US-10-215-297-4	Sequence 4, Appli
248	4	13.3	33	15	US-10-215-298-4	Sequence 4, Appli
249	4	13.3	33	15	US-10-081-816-110	Sequence 110, App
250	4	13.3	33	15	US-10-023-282-368	Sequence 368, App
251	4	13.3	34	9	US-09-864-761-44185	Sequence 44185, A
252	4	13.3	34	9	US-09-864-761-44916	Sequence 44916, A
253	4	13.3	34	9	US-09-864-761-45430	Sequence 45430, A
254	4	13.3	34	9	US-09-864-761-48511	Sequence 48511, A
255	4	13.3	34	12	US-10-231-417-538	Sequence 538, App
256	4	13.3	34	12	US-10-029-386-27795	Sequence 27795, A
257	4	13.3	34	15	US-10-106-698-8037	Sequence 8037, Ap
258	4	13.3	35	9	US-09-925-299-1258	Sequence 1258, Ap
259	4	13.3	35	10	US-09-811-824-7	Sequence 7, Appli
260	4	13.3	35	11	US-09-983-802-486	Sequence 486, App
261	4	13.3	35	11	US-09-820-843A-106	Sequence 106, App
262	4	13.3	35	11	US-09-925-299-1258	Sequence 1258, Ap
263	4	13.3	35	12	US-10-289-660-75	Sequence 75, Appl
264	4	13.3	35	12	US-10-340-484-13	Sequence 13, Appl
265	4	13.3	35	12	US-10-012-952A-147	Sequence 147, App
266	4	13.3	35	12	US-10-062-599-138	Sequence 138, App
267	4	13.3	35	15	US-10-133-128-75	Sequence 75, Appl
268	4	13.3	35	15	US-10-062-831-138	Sequence 138, App
269	4	13.3	36	8	US-08-851-965-24	Sequence 24, Appl
270	4	13.3	36	9	US-09-864-761-34257	Sequence 34257, A
271	4	13.3	36	9	US-09-864-761-39771	Sequence 39771, A
272	4	13.3	36	9	US-09-864-761-46707	Sequence 46707, A
273	4	13.3	36	9	US-09-864-761-48628	Sequence 48628, A
274	4	13.3	36	10	US-09-454-533-30	Sequence 30, Appl
275	4	13.3	36	12	US-10-340-484-12	Sequence 12, Appl
276	4	13.3	36	14	US-10-002-344A-205	Sequence 205, App
277	4	13.3	36	15	US-10-050-704-192	Sequence 192, App
278	4	13.3	37	8	US-08-851-965-22	Sequence 22, Appl
279	4	13.3	37	8	US-08-851-965-23	Sequence 23, Appl
280	4	13.3	37	8	US-08-851-965-25	Sequence 25, Appl
281	4	13.3	37	8	US-08-851-965-26	Sequence 26, Appl
282	4	13.3	37	8	US-08-851-965-27	Sequence 27, Appl
283	4	13.3	37	9	US-09-864-761-38287	Sequence 38287, A
284	4	13.3	37	9	US-09-864-761-41884	Sequence 41884, A

285	4	13.3	37	9	US-09-864-761-42087	Sequence 42087, A
286	4	13.3	37	10	US-09-908-805B-79	Sequence 79, Appl
287	4	13.3	37	10	US-09-454-533-6	Sequence 6, Appli
288	4	13.3	37	10	US-09-454-533-28	Sequence 28, Appl
289	4	13.3	37	10	US-09-454-533-29	Sequence 29, Appl
290	4	13.3	37	10	US-09-454-533-31	Sequence 31, Appl
291	4	13.3	37	10	US-09-454-533-32	Sequence 32, Appl
292	4	13.3	37	10	US-09-454-533-33	Sequence 33, Appl
293	4	13.3	37	11	US-09-764-872-347	Sequence 347, App
294	4	13.3	37	12	US-10-012-952A-209	Sequence 209, App
295	4	13.3	37	12	US-10-339-740-265	Sequence 265, App
296	4	13.3	37	12	US-10-283-403-9	Sequence 9, Appli
297	4	13.3	37	12	US-10-370-570-10	Sequence 10, Appl
298	4	13.3	37	15	US-10-082-830-161	Sequence 161, App
299	4	13.3	37	15	US-10-106-698-6085	Sequence 6085, Ap
300	4	13.3	38	9	US-09-250-883-21	Sequence 21, Appl
301	4	13.3	38	9	US-09-864-761-34617	Sequence 34617, A
302	4	13.3	38	9	US-09-864-761-38489	Sequence 38489, A
303	4	13.3	38	9	US-09-864-761-42372	Sequence 42372, A
304	4	13.3	38	9	US-09-864-761-44123	Sequence 44123, A
305	4	13.3	38	9	US-09-864-761-44436	Sequence 44436, A
306	4	13.3	39	9	US-09-864-761-41089	Sequence 41089, A
307	4	13.3	39	9	US-09-864-761-41410	Sequence 41410, A
308	4	13.3	39	10	US-09-003-869-25	Sequence 25, Appl
309	4	13.3	39	11	US-09-983-802-384	Sequence 384, App
310	4	13.3	39	11	US-09-756-690A-25	Sequence 25, Appl
311	4	13.3	39	15	US-10-157-224A-25	Sequence 25, Appl
312	4	13.3	39	15	US-10-187-051-25	Sequence 25, Appl
313	4	13.3	39	15	US-10-106-698-7822	Sequence 7822, Ap
314	4	13.3	40	11	US-09-764-891-2762	Sequence 2762, Ap
315	4	13.3	40	12	US-10-058-053A-81	Sequence 81, Appl
316	4	13.3	40	12	US-10-058-053A-264	Sequence 264, App
317	4	13.3	40	15	US-10-091-572-223	Sequence 223, App
318	3	10.0	28	8	US-08-908-884-7	Sequence 7, Appli
319	3	10.0	28	9	US-09-799-983-16	Sequence 16, Appl
320	3	10.0	28	9	US-09-799-983-18	Sequence 18, Appl
321	3	10.0	28	9	US-09-730-379B-10	Sequence 10, Appl
322	3	10.0	28	9	US-09-765-527-30	Sequence 30, Appl
323	3	10.0	28	9	US-09-765-527-139	Sequence 139, App
324	3	10.0	28	9	US-09-765-527-140	Sequence 140, App
325	3	10.0	28	9	US-09-765-527-142	Sequence 142, App
326	3	10.0	28	9	US-09-765-527-143	Sequence 143, App
327	3	10.0	28	9	US-09-895-072-27	Sequence 27, Appl
328	3	10.0	28	9	US-09-864-761-33837	Sequence 33837, A
329	3	10.0	28	9	US-09-864-761-34933	Sequence 34933, A
330	3	10.0	28	9	US-09-864-761-34971	Sequence 34971, A
331	3	10.0	28	9	US-09-864-761-35640	Sequence 35640, A
332	3	10.0	28	9	US-09-864-761-35827	Sequence 35827, A
333	3	10.0	28	9	US-09-864-761-36728	Sequence 36728, A
334	3	10.0	28	9	US-09-864-761-37848	Sequence 37848, A
335	3	10.0	28	9	US-09-864-761-37919	Sequence 37919, A
336	3	10.0	28	9	US-09-864-761-37927	Sequence 37927, A
337	3	10.0	28	9	US-09-864-761-39084	Sequence 39084, A
338	3	10.0	28	9	US-09-864-761-39493	Sequence 39493, A
339	3	10.0	28	9	US-09-864-761-39762	Sequence 39762, A
340	3	10.0	28	9	US-09-864-761-39984	Sequence 39984, A
341	3	10.0	28	9	US-09-864-761-40300	Sequence 40300, A

342	3	10.0	28	9	US-09-864-761-41015	Sequence 41015, A
343	3	10.0	28	9	US-09-864-761-41850	Sequence 41850, A
344	3	10.0	28	9	US-09-864-761-42022	Sequence 42022, A
345	3	10.0	28	9	US-09-864-761-42177	Sequence 42177, A
346	3	10.0	28	9	US-09-864-761-42253	Sequence 42253, A
347	3	10.0	28	9	US-09-864-761-43275	Sequence 43275, A
348	3	10.0	28	9	US-09-864-761-43834	Sequence 43834, A
349	3	10.0	28	9	US-09-864-761-43979	Sequence 43979, A
350	3	10.0	28	9	US-09-864-761-44041	Sequence 44041, A
351	3	10.0	28	9	US-09-864-761-44733	Sequence 44733, A
352	3	10.0	28	9	US-09-864-761-45427	Sequence 45427, A
353	3	10.0	28	9	US-09-864-761-46128	Sequence 46128, A
354	3	10.0	28	9	US-09-864-761-47128	Sequence 47128, A
355	3	10.0	28	9	US-09-864-761-47465	Sequence 47465, A
356	3	10.0	28	9	US-09-864-761-47968	Sequence 47968, A
357	3	10.0	28	9	US-09-864-761-48171	Sequence 48171, A
358	3	10.0	28	9	US-09-864-761-48316	Sequence 48316, A
359	3	10.0	28	9	US-09-962-055-26	Sequence 26, Appl
360	3	10.0	28	9	US-09-925-301-1524	Sequence 1524, Ap
361	3	10.0	28	9	US-09-925-299-1173	Sequence 1173, Ap
362	3	10.0	28	9	US-09-728-721-19	Sequence 19, Appl
363	3	10.0	28	9	US-09-728-721-23	Sequence 23, Appl
364	3	10.0	28	9	US-09-908-323-7	Sequence 7, Appli
365	3	10.0	28	9	US-09-881-490-5	Sequence 5, Appli
366	3	10.0	28	9	US-09-881-490-110	Sequence 110, App
367	3	10.0	28	9	US-09-881-490-111	Sequence 111, App
368	3	10.0	28	9	US-09-881-490-113	Sequence 113, App
369	3	10.0	28	9	US-09-881-490-114	Sequence 114, App
370	3	10.0	28	9	US-09-879-666-4	Sequence 4, Appli
371	3	10.0	28	9	US-09-929-818-1	Sequence 1, Appli
372	3	10.0	28	9	US-09-929-818-2	Sequence 2, Appli
373	3	10.0	28	9	US-09-929-818-3	Sequence 3, Appli
374	3	10.0	28	9	US-09-929-818-4	Sequence 4, Appli
375	3	10.0	28	9	US-09-929-818-5	Sequence 5, Appli
376	3	10.0	28	9	US-09-929-818-6	Sequence 6, Appli
377	3	10.0	28	9	US-09-929-818-7	Sequence 7, Appli
378	3	10.0	28	9	US-09-929-818-8	Sequence 8, Appli
379	3	10.0	28	9	US-09-929-818-9	Sequence 9, Appli
380	3	10.0	28	9	US-09-929-818-10	Sequence 10, Appl
381	3	10.0	28	9	US-09-929-818-11	Sequence 11, Appl
382	3	10.0	28	9	US-09-929-818-12	Sequence 12, Appl
383	3	10.0	28	9	US-09-929-818-13	Sequence 13, Appl
384	3	10.0	28	9	US-09-929-818-14	Sequence 14, Appl
385	3	10.0	28	9	US-09-929-818-15	Sequence 15, Appl
386	3	10.0	28	9	US-09-929-818-16	Sequence 16, Appl
387	3	10.0	28	9	US-09-929-818-17	Sequence 17, Appl
388	3	10.0	28	9	US-09-929-818-18	Sequence 18, Appl
389	3	10.0	28	9	US-09-929-818-19	Sequence 19, Appl
390	3	10.0	28	9	US-09-929-818-20	Sequence 20, Appl
391	3	10.0	28	9	US-09-929-818-21	Sequence 21, Appl
392	3	10.0	28	9	US-09-929-818-22	Sequence 22, Appl
393	3	10.0	28	9	US-09-929-818-23	Sequence 23, Appl
394	3	10.0	28	9	US-09-929-818-24	Sequence 24, Appl
395	3	10.0	28	9	US-09-929-818-25	Sequence 25, Appl
396	3	10.0	28	9	US-09-929-818-26	Sequence 26, Appl
397	3	10.0	28	9	US-09-929-818-27	Sequence 27, Appl
398	3	10.0	28	9	US-09-929-818-28	Sequence 28, Appl

399	3	10.0	28	9	US-09-929-818-29	Sequence 29, Appl
400	3	10.0	28	9	US-09-929-818-30	Sequence 30, Appl
401	3	10.0	28	9	US-09-929-818-31	Sequence 31, Appl
402	3	10.0	28	9	US-09-929-818-32	Sequence 32, Appl
403	3	10.0	28	9	US-09-929-818-33	Sequence 33, Appl
404	3	10.0	28	9	US-09-929-818-34	Sequence 34, Appl
405	3	10.0	28	9	US-09-929-818-35	Sequence 35, Appl
406	3	10.0	28	9	US-09-929-818-36	Sequence 36, Appl
407	3	10.0	28	9	US-09-929-818-37	Sequence 37, Appl
408	3	10.0	28	9	US-09-929-818-38	Sequence 38, Appl
409	3	10.0	28	9	US-09-929-818-39	Sequence 39, Appl
410	3	10.0	28	9	US-09-929-818-40	Sequence 40, Appl
411	3	10.0	28	9	US-09-929-818-41	Sequence 41, Appl
412	3	10.0	28	9	US-09-929-818-42	Sequence 42, Appl
413	3	10.0	28	9	US-09-929-818-43	Sequence 43, Appl
414	3	10.0	28	9	US-09-929-818-44	Sequence 44, Appl
415	3	10.0	28	9	US-09-929-818-45	Sequence 45, Appl
416	3	10.0	28	9	US-09-929-818-46	Sequence 46, Appl
417	3	10.0	28	9	US-09-929-818-47	Sequence 47, Appl
418	3	10.0	28	9	US-09-929-818-48	Sequence 48, Appl
419	3	10.0	28	9	US-09-929-818-49	Sequence 49, Appl
420	3	10.0	28	9	US-09-929-818-50	Sequence 50, Appl
421	3	10.0	28	9	US-09-929-818-51	Sequence 51, Appl
422	3	10.0	28	9	US-09-929-818-52	Sequence 52, Appl
423	3	10.0	28	9	US-09-929-818-53	Sequence 53, Appl
424	3	10.0	28	9	US-09-929-818-54	Sequence 54, Appl
425	3	10.0	28	9	US-09-929-818-61	Sequence 61, Appl
426	3	10.0	28	9	US-09-929-818-62	Sequence 62, Appl
427	3	10.0	28	9	US-09-929-818-66	Sequence 66, Appl
428	3	10.0	28	9	US-09-929-818-69	Sequence 69, Appl
429	3	10.0	28	9	US-09-929-818-76	Sequence 76, Appl
430	3	10.0	28	9	US-09-929-818-77	Sequence 77, Appl
431	3	10.0	28	9	US-09-929-818-80	Sequence 80, Appl
432	3	10.0	28	9	US-09-929-818-87	Sequence 87, Appl
433	3	10.0	28	9	US-09-929-818-94	Sequence 94, Appl
434	3	10.0	28	9	US-09-929-818-95	Sequence 95, Appl
435	3	10.0	28	9	US-09-929-818-97	Sequence 97, Appl
436	3	10.0	28	9	US-09-929-818-99	Sequence 99, Appl
437	3	10.0	28	9	US-09-929-818-100	Sequence 100, App
438	3	10.0	28	9	US-09-929-818-101	Sequence 101, App
439	3	10.0	28	9	US-09-929-818-102	Sequence 102, App
440	3	10.0	28	9	US-09-929-818-103	Sequence 103, App
441	3	10.0	28	9	US-09-929-818-104	Sequence 104, App
442	3	10.0	28	9	US-09-929-818-105	Sequence 105, App
443	3	10.0	28	9	US-09-929-818-106	Sequence 106, App
444	3	10.0	28	9	US-09-929-818-107	Sequence 107, App
445	3	10.0	28	9	US-09-929-818-108	Sequence 108, App
446	3	10.0	28	9	US-09-929-818-109	Sequence 109, App
447	3	10.0	28	9	US-09-929-818-110	Sequence 110, App
448	3	10.0	28	9	US-09-929-818-111	Sequence 111, App
449	3	10.0	28	9	US-09-929-818-112	Sequence 112, App
450	3	10.0	28	9	US-09-929-818-113	Sequence 113, App
451	3	10.0	28	9	US-09-929-818-114	Sequence 114, App
452	3	10.0	28	9	US-09-929-818-115	Sequence 115, App
453	3	10.0	28	9	US-09-929-818-116	Sequence 116, App
454	3	10.0	28	9	US-09-929-818-117	Sequence 117, App
455	3	10.0	28	9	US-09-929-818-118	Sequence 118, App

456	3	10.0	28	9	US-09-929-818-119	Sequence 119, App
457	3	10.0	28	9	US-09-929-818-120	Sequence 120, App
458	3	10.0	28	9	US-09-929-818-121	Sequence 121, App
459	3	10.0	28	9	US-09-929-818-123	Sequence 123, App
460	3	10.0	28	9	US-09-929-818-124	Sequence 124, App
461	3	10.0	28	9	US-09-929-818-125	Sequence 125, App
462	3	10.0	28	9	US-09-929-818-126	Sequence 126, App
463	3	10.0	28	9	US-09-929-818-127	Sequence 127, App
464	3	10.0	28	9	US-09-929-818-128	Sequence 128, App
465	3	10.0	28	9	US-09-929-818-129	Sequence 129, App
466	3	10.0	28	9	US-09-929-818-130	Sequence 130, App
467	3	10.0	28	9	US-09-929-818-131	Sequence 131, App
468	3	10.0	28	9	US-09-929-818-132	Sequence 132, App
469	3	10.0	28	9	US-09-929-818-133	Sequence 133, App
470	3	10.0	28	9	US-09-929-818-134	Sequence 134, App
471	3	10.0	28	9	US-09-929-818-135	Sequence 135, App
472	3	10.0	28	9	US-09-929-818-136	Sequence 136, App
473	3	10.0	28	9	US-09-929-818-137	Sequence 137, App
474	3	10.0	28	9	US-09-929-818-138	Sequence 138, App
475	3	10.0	28	9	US-09-929-818-139	Sequence 139, App
476	3	10.0	28	9	US-09-929-818-140	Sequence 140, App
477	3	10.0	28	9	US-09-929-818-141	Sequence 141, App
478	3	10.0	28	9	US-09-929-818-142	Sequence 142, App
479	3	10.0	28	9	US-09-929-818-143	Sequence 143, App
480	3	10.0	28	9	US-09-929-818-144	Sequence 144, App
481	3	10.0	28	9	US-09-929-818-145	Sequence 145, App
482	3	10.0	28	9	US-09-929-818-146	Sequence 146, App
483	3	10.0	28	9	US-09-929-818-147	Sequence 147, App
484	3	10.0	28	9	US-09-929-818-148	Sequence 148, App
485	3	10.0	28	9	US-09-929-818-149	Sequence 149, App
486	3	10.0	28	9	US-09-929-818-150	Sequence 150, App
487	3	10.0	28	9	US-09-929-818-151	Sequence 151, App
488	3	10.0	28	9	US-09-929-818-152	Sequence 152, App
489	3	10.0	28	9	US-09-929-818-153	Sequence 153, App
490	3	10.0	28	9	US-09-929-818-154	Sequence 154, App
491	3	10.0	28	9	US-09-929-818-155	Sequence 155, App
492	3	10.0	28	9	US-09-929-818-156	Sequence 156, App
493	3	10.0	28	9	US-09-929-818-157	Sequence 157, App
494	3	10.0	28	9	US-09-929-818-158	Sequence 158, App
495	3	10.0	28	9	US-09-929-818-159	Sequence 159, App
496	3	10.0	28	9	US-09-929-818-160	Sequence 160, App
497	3	10.0	28	9	US-09-929-818-161	Sequence 161, App
498	3	10.0	28	9	US-09-929-818-162	Sequence 162, App
499	3	10.0	28	9	US-09-929-818-163	Sequence 163, App
500	3	10.0	28	9	US-09-929-818-164	Sequence 164, App
501	3	10.0	28	9	US-09-929-818-165	Sequence 165, App
502	3	10.0	28	9	US-09-929-818-166	Sequence 166, App
503	3	10.0	28	9	US-09-929-818-167	Sequence 167, App
504	3	10.0	28	9	US-09-929-818-168	Sequence 168, App
505	3	10.0	28	9	US-09-929-818-169	Sequence 169, App
506	3	10.0	28	9	US-09-929-818-170	Sequence 170, App
507	3	10.0	28	9	US-09-929-818-171	Sequence 171, App
508	3	10.0	28	9	US-09-929-818-172	Sequence 172, App
509	3	10.0	28	9	US-09-929-818-173	Sequence 173, App
510	3	10.0	28	9	US-09-929-818-174	Sequence 174, App
511	3	10.0	28	9	US-09-929-818-175	Sequence 175, App
512	3	10.0	28	9	US-09-929-818-176	Sequence 176, App

513	3	10.0	28	9	US-09-929-818-177	Sequence 177, App
514	3	10.0	28	9	US-09-929-818-178	Sequence 178, App
515	3	10.0	28	9	US-09-929-818-179	Sequence 179, App
516	3	10.0	28	9	US-09-929-818-180	Sequence 180, App
517	3	10.0	28	9	US-09-929-818-181	Sequence 181, App
518	3	10.0	28	9	US-09-929-818-182	Sequence 182, App
519	3	10.0	28	9	US-09-929-818-183	Sequence 183, App
520	3	10.0	28	9	US-09-929-818-184	Sequence 184, App
521	3	10.0	28	9	US-09-929-818-185	Sequence 185, App
522	3	10.0	28	9	US-09-929-818-186	Sequence 186, App
523	3	10.0	28	9	US-09-929-818-187	Sequence 187, App
524	3	10.0	28	9	US-09-929-818-188	Sequence 188, App
525	3	10.0	28	9	US-09-929-818-189	Sequence 189, App
526	3	10.0	28	9	US-09-929-818-190	Sequence 190, App
527	3	10.0	28	9	US-09-929-818-191	Sequence 191, App
528	3	10.0	28	9	US-09-929-818-192	Sequence 192, App
529	3	10.0	28	9	US-09-929-818-193	Sequence 193, App
530	3	10.0	28	9	US-09-929-818-194	Sequence 194, App
531	3	10.0	28	9	US-09-929-818-195	Sequence 195, App
532	3	10.0	28	9	US-09-929-818-196	Sequence 196, App
533	3	10.0	28	9	US-09-929-818-197	Sequence 197, App
534	3	10.0	28	9	US-09-929-818-198	Sequence 198, App
535	3	10.0	28	9	US-09-929-818-199	Sequence 199, App
536	3	10.0	28	9	US-09-929-818-201	Sequence 201, App
537	3	10.0	28	9	US-09-929-818-202	Sequence 202, App
538	3	10.0	28	9	US-09-929-818-207	Sequence 207, App
539	3	10.0	28	10	US-09-117-380B-4	Sequence 4, Appli
540	3	10.0	28	10	US-09-003-869-40	Sequence 40, Appl
541	3	10.0	28	10	US-09-003-869-90	Sequence 90, Appl
542	3	10.0	28	10	US-09-003-869-91	Sequence 91, Appl
543	3	10.0	28	10	US-09-003-869-92	Sequence 92, Appl
544	3	10.0	28	10	US-09-003-869-95	Sequence 95, Appl
545	3	10.0	28	10	US-09-003-869-104	Sequence 104, App
546	3	10.0	28	10	US-09-003-869-105	Sequence 105, App
547	3	10.0	28	10	US-09-003-869-106	Sequence 106, App
548	3	10.0	28	10	US-09-003-869-107	Sequence 107, App
549	3	10.0	28	10	US-09-003-869-108	Sequence 108, App
550	3	10.0	28	10	US-09-003-869-109	Sequence 109, App
551	3	10.0	28	10	US-09-003-869-111	Sequence 111, App
552	3	10.0	28	10	US-09-003-869-113	Sequence 113, App
553	3	10.0	28	10	US-09-003-869-115	Sequence 115, App
554	3	10.0	28	10	US-09-003-869-117	Sequence 117, App
555	3	10.0	28	10	US-09-003-869-119	Sequence 119, App
556	3	10.0	28	10	US-09-003-869-121	Sequence 121, App
557	3	10.0	28	10	US-09-003-869-123	Sequence 123, App
558	3	10.0	28	10	US-09-003-869-125	Sequence 125, App
559	3	10.0	28	10	US-09-003-869-127	Sequence 127, App
560	3	10.0	28	10	US-09-003-869-129	Sequence 129, App
561	3	10.0	28	10	US-09-003-869-131	Sequence 131, App
562	3	10.0	28	10	US-09-003-869-133	Sequence 133, App
563	3	10.0	28	10	US-09-003-869-135	Sequence 135, App
564	3	10.0	28	10	US-09-003-869-137	Sequence 137, App
565	3	10.0	28	10	US-09-003-869-139	Sequence 139, App
566	3	10.0	28	10	US-09-003-869-141	Sequence 141, App
567	3	10.0	28	10	US-09-003-869-143	Sequence 143, App
568	3	10.0	28	10	US-09-003-869-145	Sequence 145, App
569	3	10.0	28	10	US-09-003-869-147	Sequence 147, App

570	3	10.0	28	10	US-09-003-869-149	Sequence 149, App
571	3	10.0	28	10	US-09-003-869-151	Sequence 151, App
572	3	10.0	28	10	US-09-003-869-155	Sequence 155, App
573	3	10.0	28	10	US-09-003-869-163	Sequence 163, App
574	3	10.0	28	10	US-09-003-869-165	Sequence 165, App
575	3	10.0	28	10	US-09-903-456-116	Sequence 116, App
576	3	10.0	28	10	US-09-989-903-23	Sequence 23, Appl
577	3	10.0	28	10	US-09-986-552-27	Sequence 27, Appl
578	3	10.0	28	10	US-09-934-060A-20	Sequence 20, Appl
579	3	10.0	28	10	US-09-999-745-53	Sequence 53, Appl
580	3	10.0	28	10	US-09-981-876-241	Sequence 241, App
581	3	10.0	28	10	US-09-880-498-1	Sequence 1, Appli
582	3	10.0	28	10	US-09-554-000-37	Sequence 37, Appl
583	3	10.0	28	10	US-09-848-967-3	Sequence 3, Appli
584	3	10.0	28	10	US-09-848-967-4	Sequence 4, Appli
585	3	10.0	28	10	US-09-976-740-26	Sequence 26, Appl
586	3	10.0	28	11	US-09-983-802-481	Sequence 481, App
587	3	10.0	28	11	US-09-983-802-531	Sequence 531, App
588	3	10.0	28	11	US-09-999-724-28	Sequence 28, Appl
589	3	10.0	28	11	US-09-148-545-241	Sequence 241, App
590	3	10.0	28	11	US-09-974-879-269	Sequence 269, App
591	3	10.0	28	11	US-09-974-879-520	Sequence 520, App
592	3	10.0	28	11	US-09-974-879-543	Sequence 543, App
593	3	10.0	28	11	US-09-974-879-579	Sequence 579, App
594	3	10.0	28	11	US-09-756-690A-40	Sequence 40, Appl
595	3	10.0	28	11	US-09-756-690A-90	Sequence 90, Appl
596	3	10.0	28	11	US-09-756-690A-91	Sequence 91, Appl
597	3	10.0	28	11	US-09-756-690A-92	Sequence 92, Appl
598	3	10.0	28	11	US-09-756-690A-95	Sequence 95, Appl
599	3	10.0	28	11	US-09-756-690A-104	Sequence 104, App
600	3	10.0	28	11	US-09-756-690A-105	Sequence 105, App
601	3	10.0	28	11	US-09-756-690A-106	Sequence 106, App
602	3	10.0	28	11	US-09-756-690A-107	Sequence 107, App
603	3	10.0	28	11	US-09-756-690A-108	Sequence 108, App
604	3	10.0	28	11	US-09-756-690A-109	Sequence 109, App
605	3	10.0	28	11	US-09-756-690A-111	Sequence 111, App
606	3	10.0	28	11	US-09-756-690A-113	Sequence 113, App
607	3	10.0	28	11	US-09-756-690A-115	Sequence 115, App
608	3	10.0	28	11	US-09-756-690A-117	Sequence 117, App
609	3	10.0	28	11	US-09-756-690A-119	Sequence 119, App
610	3	10.0	28	11	US-09-756-690A-121	Sequence 121, App
611	3	10.0	28	11	US-09-756-690A-123	Sequence 123, App
612	3	10.0	28	11	US-09-756-690A-125	Sequence 125, App
613	3	10.0	28	11	US-09-756-690A-127	Sequence 127, App
614	3	10.0	28	11	US-09-756-690A-129	Sequence 129, App
615	3	10.0	28	11	US-09-756-690A-131	Sequence 131, App
616	3	10.0	28	11	US-09-756-690A-133	Sequence 133, App
617	3	10.0	28	11	US-09-756-690A-135	Sequence 135, App
618	3	10.0	28	11	US-09-756-690A-137	Sequence 137, App
619	3	10.0	28	11	US-09-756-690A-139	Sequence 139, App
620	3	10.0	28	11	US-09-756-690A-141	Sequence 141, App
621	3	10.0	28	11	US-09-756-690A-143	Sequence 143, App
622	3	10.0	28	11	US-09-756-690A-145	Sequence 145, App
623	3	10.0	28	11	US-09-756-690A-147	Sequence 147, App
624	3	10.0	28	11	US-09-756-690A-149	Sequence 149, App
625	3	10.0	28	11	US-09-756-690A-151	Sequence 151, App
626	3	10.0	28	11	US-09-756-690A-155	Sequence 155, App

627	3	10.0	28	11	US-09-756-690A-163	Sequence 163, App
628	3	10.0	28	11	US-09-756-690A-165	Sequence 165, App
629	3	10.0	28	11	US-09-843-221A-72	Sequence 72, Appl
630	3	10.0	28	11	US-09-843-221A-75	Sequence 75, Appl
631	3	10.0	28	11	US-09-843-221A-104	Sequence 104, App
632	3	10.0	28	11	US-09-925-299-1173	Sequence 1173, Ap
633	3	10.0	28	11	US-09-945-917-23	Sequence 23, Appl
634	3	10.0	28	11	US-09-813-153-220	Sequence 220, App
635	3	10.0	28	11	US-09-876-904A-230	Sequence 230, App
636	3	10.0	28	11	US-09-892-877-335	Sequence 335, App
637	3	10.0	28	11	US-09-910-180-19	Sequence 19, Appl
638	3	10.0	28	11	US-09-305-736-285	Sequence 285, App
639	3	10.0	28	11	US-09-305-736-522	Sequence 522, App
640	3	10.0	28	11	US-09-305-736-545	Sequence 545, App
641	3	10.0	28	11	US-09-305-736-580	Sequence 580, App
642	3	10.0	28	11	US-09-948-783-348	Sequence 348, App
643	3	10.0	28	11	US-09-866-066-31	Sequence 31, Appl
644	3	10.0	28	12	US-10-195-730-307	Sequence 307, App
645	3	10.0	28	12	US-10-195-730-354	Sequence 354, App
646	3	10.0	28	12	US-10-309-422-4	Sequence 4, Appli
647	3	10.0	28	12	US-10-334-405-4	Sequence 4, Appli
648	3	10.0	28	12	US-10-251-703-21	Sequence 21, Appl
649	3	10.0	28	12	US-10-306-686-27	Sequence 27, Appl
650	3	10.0	28	12	US-09-991-225-35	Sequence 35, Appl
651	3	10.0	28	12	US-10-100-256B-1	Sequence 1, Appli
652	3	10.0	28	12	US-10-254-569A-1	Sequence 1, Appli
653	3	10.0	28	12	US-10-254-569A-2	Sequence 2, Appli
654	3	10.0	28	12	US-10-254-569A-3	Sequence 3, Appli
655	3	10.0	28	12	US-10-254-569A-4	Sequence 4, Appli
656	3	10.0	28	12	US-10-254-569A-5	Sequence 5, Appli
657	3	10.0	28	12	US-10-254-569A-6	Sequence 6, Appli
658	3	10.0	28	12	US-10-254-569A-7	Sequence 7, Appli
659	3	10.0	28	12	US-10-254-569A-8	Sequence 8, Appli
660	3	10.0	28	12	US-10-254-569A-9	Sequence 9, Appli
661	3	10.0	28	12	US-10-254-569A-10	Sequence 10, Appl
662	3	10.0	28	12	US-10-254-569A-11	Sequence 11, Appl
663	3	10.0	28	12	US-10-254-569A-12	Sequence 12, Appl
664	3	10.0	28	12	US-10-156-911-116	Sequence 116, App
665	3	10.0	28	12	US-09-845-917A-23	Sequence 23, Appl
666	3	10.0	28	12	US-10-322-746-7	Sequence 7, Appli
667	3	10.0	28	12	US-10-411-224-108	Sequence 108, App
668	3	10.0	28	12	US-09-829-922-22	Sequence 22, Appl
669	3	10.0	28	12	US-10-231-417-591	Sequence 591, App
670	3	10.0	28	12	US-10-312-691-2	Sequence 2, Appli
671	3	10.0	28	12	US-10-314-506-16	Sequence 16, Appl
672	3	10.0	28	12	US-10-314-506-17	Sequence 17, Appl
673	3	10.0	28	12	US-10-408-736-81	Sequence 81, Appl
674	3	10.0	28	12	US-09-933-767-626	Sequence 626, App
675	3	10.0	28	12	US-09-933-767-638	Sequence 638, App
676	3	10.0	28	12	US-09-933-767-1089	Sequence 1089, Ap
677	3	10.0	28	12	US-10-105-232-329	Sequence 329, App
678	3	10.0	28	12	US-10-131-686A-19	Sequence 19, Appl
679	3	10.0	28	12	US-10-289-135A-36	Sequence 36, Appl
680	3	10.0	28	12	US-10-276-392-1	Sequence 1, Appli
681	3	10.0	28	12	US-10-276-392-7	Sequence 7, Appli
682	3	10.0	28	12	US-10-276-392-8	Sequence 8, Appli
683	3	10.0	28	12	US-10-276-392-9	Sequence 9, Appli

684	3	10.0	28	12	US-10-276-392-10	Sequence 10, Appl
685	3	10.0	28	12	US-10-276-392-11	Sequence 11, Appl
686	3	10.0	28	12	US-10-276-392-12	Sequence 12, Appl
687	3	10.0	28	12	US-10-276-392-13	Sequence 13, Appl
688	3	10.0	28	12	US-10-276-392-14	Sequence 14, Appl
689	3	10.0	28	12	US-10-276-392-15	Sequence 15, Appl
690	3	10.0	28	12	US-10-276-392-16	Sequence 16, Appl
691	3	10.0	28	12	US-10-276-392-17	Sequence 17, Appl
692	3	10.0	28	12	US-10-276-392-18	Sequence 18, Appl
693	3	10.0	28	12	US-10-276-392-19	Sequence 19, Appl
694	3	10.0	28	12	US-10-276-392-20	Sequence 20, Appl
695	3	10.0	28	12	US-10-276-392-21	Sequence 21, Appl
696	3	10.0	28	12	US-10-330-872-9	Sequence 9, Appli
697	3	10.0	28	12	US-10-351-641-54	Sequence 54, Appl
698	3	10.0	28	12	US-10-351-641-62	Sequence 62, Appl
699	3	10.0	28	12	US-10-351-641-1279	Sequence 1279, Ap
700	3	10.0	28	12	US-10-351-641-1280	Sequence 1280, Ap
701	3	10.0	28	12	US-10-351-641-1314	Sequence 1314, Ap
702	3	10.0	28	12	US-10-351-641-1315	Sequence 1315, Ap
703	3	10.0	28	12	US-10-029-386-27986	Sequence 27986, A
704	3	10.0	28	12	US-10-029-386-28154	Sequence 28154, A
705	3	10.0	28	12	US-10-029-386-28548	Sequence 28548, A
706	3	10.0	28	12	US-10-029-386-31090	Sequence 31090, A
707	3	10.0	28	12	US-10-029-386-31138	Sequence 31138, A
708	3	10.0	28	12	US-10-029-386-31267	Sequence 31267, A
709	3	10.0	28	12	US-10-029-386-31429	Sequence 31429, A
710	3	10.0	28	12	US-10-029-386-33289	Sequence 33289, A
711	3	10.0	28	12	US-10-029-386-33582	Sequence 33582, A
712	3	10.0	28	12	US-10-189-437-316	Sequence 316, App
713	3	10.0	28	12	US-10-189-437-669	Sequence 669, App
714	3	10.0	28	12	US-10-080-254-100	Sequence 100, App
715	3	10.0	28	12	US-10-080-608A-1	Sequence 1, Appli
716	3	10.0	28	12	US-09-818-683-285	Sequence 285, App
717	3	10.0	28	12	US-09-818-683-522	Sequence 522, App
718	3	10.0	28	12	US-09-818-683-545	Sequence 545, App
719	3	10.0	28	12	US-09-818-683-580	Sequence 580, App
720	3	10.0	28	12	US-10-370-685-90	Sequence 90, Appl
721	3	10.0	28	12	US-09-873-155-43	Sequence 43, Appl
722	3	10.0	28	12	US-10-366-493-24	Sequence 24, Appl
723	3	10.0	28	12	US-10-391-399-86	Sequence 86, Appl
724	3	10.0	28	12	US-10-211-689-8	Sequence 8, Appli
725	3	10.0	28	12	US-10-324-143-148	Sequence 148, App
726	3	10.0	28	12	US-10-242-355-646	Sequence 646, App
727	3	10.0	28	12	US-10-245-871-32	Sequence 32, Appl
728	3	10.0	28	12	US-10-154-884B-11082	Sequence 11082, A
729	3	10.0	28	12	US-10-264-049-2573	Sequence 2573, Ap
730	3	10.0	28	12	US-10-264-049-3158	Sequence 3158, Ap
731	3	10.0	28	14	US-10-014-269-16	Sequence 16, Appl
732	3	10.0	28	14	US-10-014-269-17	Sequence 17, Appl
733	3	10.0	28	14	US-10-023-529-26	Sequence 26, Appl
734	3	10.0	28	14	US-10-105-931-19	Sequence 19, Appl
735	3	10.0	28	14	US-10-105-931-23	Sequence 23, Appl
736	3	10.0	28	14	US-10-090-109A-1	Sequence 1, Appli
737	3	10.0	28	14	US-10-023-523-26	Sequence 26, Appl
738	3	10.0	28	14	US-10-044-722-8	Sequence 8, Appli
739	3	10.0	28	14	US-10-002-974-16	Sequence 16, Appl
740	3	10.0	28	14	US-10-002-974-17	Sequence 17, Appl

741	3	10.0	28	14	US-10-118-984-19	Sequence 19, Appl
742	3	10.0	28	14	US-10-118-984-23	Sequence 23, Appl
743	3	10.0	28	15	US-10-014-162-48	Sequence 48, Appl
744	3	10.0	28	15	US-10-000-256A-219	Sequence 219, App
745	3	10.0	28	15	US-10-068-564-23	Sequence 23, Appl
746	3	10.0	28	15	US-10-078-090-126	Sequence 126, App
747	3	10.0	28	15	US-10-004-530A-17	Sequence 17, Appl
748	3	10.0	28	15	US-10-131-433-6	Sequence 6, Appli
749	3	10.0	28	15	US-10-097-065-486	Sequence 486, App
750	3	10.0	28	15	US-10-097-065-598	Sequence 598, App
751	3	10.0	28	15	US-10-059-261-324	Sequence 324, App
752	3	10.0	28	15	US-10-150-111-131	Sequence 131, App
753	3	10.0	28	15	US-10-211-994-1	Sequence 1, Appli
754	3	10.0	28	15	US-10-157-224A-40	Sequence 40, Appl
755	3	10.0	28	15	US-10-157-224A-90	Sequence 90, Appl
756	3	10.0	28	15	US-10-157-224A-91	Sequence 91, Appl
757	3	10.0	28	15	US-10-157-224A-92	Sequence 92, Appl
758	3	10.0	28	15	US-10-157-224A-95	Sequence 95, Appl
759	3	10.0	28	15	US-10-157-224A-104	Sequence 104, App
760	3	10.0	28	15	US-10-157-224A-105	Sequence 105, App
761	3	10.0	28	15	US-10-157-224A-106	Sequence 106, App
762	3	10.0	28	15	US-10-157-224A-107	Sequence 107, App
763	3	10.0	28	15	US-10-157-224A-108	Sequence 108, App
764	3	10.0	28	15	US-10-157-224A-109	Sequence 109, App
765	3	10.0	28	15	US-10-157-224A-111	Sequence 111, App
766	3	10.0	28	15	US-10-157-224A-113	Sequence 113, App
767	3	10.0	28	15	US-10-157-224A-115	Sequence 115, App
768	3	10.0	28	15	US-10-157-224A-117	Sequence 117, App
769	3	10.0	28	15	US-10-157-224A-119	Sequence 119, App
770	3	10.0	28	15	US-10-157-224A-121	Sequence 121, App
771	3	10.0	28	15	US-10-157-224A-123	Sequence 123, App
772	3	10.0	28	15	US-10-157-224A-125	Sequence 125, App
773	3	10.0	28	15	US-10-157-224A-127	Sequence 127, App
774	3	10.0	28	15	US-10-157-224A-129	Sequence 129, App
775	3	10.0	28	15	US-10-157-224A-131	Sequence 131, App
776	3	10.0	28	15	US-10-157-224A-133	Sequence 133, App
777	3	10.0	28	15	US-10-157-224A-135	Sequence 135, App
778	3	10.0	28	15	US-10-157-224A-137	Sequence 137, App
779	3	10.0	28	15	US-10-157-224A-139	Sequence 139, App
780	3	10.0	28	15	US-10-157-224A-141	Sequence 141, App
781	3	10.0	28	15	US-10-157-224A-143	Sequence 143, App
782	3	10.0	28	15	US-10-157-224A-145	Sequence 145, App
783	3	10.0	28	15	US-10-157-224A-147	Sequence 147, App
784	3	10.0	28	15	US-10-157-224A-149	Sequence 149, App
785	3	10.0	28	15	US-10-157-224A-151	Sequence 151, App
786	3	10.0	28	15	US-10-157-224A-155	Sequence 155, App
787	3	10.0	28	15	US-10-157-224A-163	Sequence 163, App
788	3	10.0	28	15	US-10-157-224A-165	Sequence 165, App
789	3	10.0	28	15	US-10-187-051-40	Sequence 40, Appl
790	3	10.0	28	15	US-10-187-051-90	Sequence 90, Appl
791	3	10.0	28	15	US-10-187-051-91	Sequence 91, Appl
792	3	10.0	28	15	US-10-187-051-92	Sequence 92, Appl
793	3	10.0	28	15	US-10-187-051-95	Sequence 95, Appl
794	3	10.0	28	15	US-10-187-051-104	Sequence 104, App
795	3	10.0	28	15	US-10-187-051-105	Sequence 105, App
796	3	10.0	28	15	US-10-187-051-106	Sequence 106, App
797	3	10.0	28	15	US-10-187-051-107	Sequence 107, App

798	3	10.0	28	15	US-10-187-051-108	Sequence 108, App
799	3	10.0	28	15	US-10-187-051-109	Sequence 109, App
800	3	10.0	28	15	US-10-187-051-111	Sequence 111, App
801	3	10.0	28	15	US-10-187-051-113	Sequence 113, App
802	3	10.0	28	15	US-10-187-051-115	Sequence 115, App
803	3	10.0	28	15	US-10-187-051-117	Sequence 117, App
804	3	10.0	28	15	US-10-187-051-119	Sequence 119, App
805	3	10.0	28	15	US-10-187-051-121	Sequence 121, App
806	3	10.0	28	15	US-10-187-051-123	Sequence 123, App
807	3	10.0	28	15	US-10-187-051-125	Sequence 125, App
808	3	10.0	28	15	US-10-187-051-127	Sequence 127, App
809	3	10.0	28	15	US-10-187-051-129	Sequence 129, App
810	3	10.0	28	15	US-10-187-051-131	Sequence 131, App
811	3	10.0	28	15	US-10-187-051-133	Sequence 133, App
812	3	10.0	28	15	US-10-187-051-135	Sequence 135, App
813	3	10.0	28	15	US-10-187-051-137	Sequence 137, App
814	3	10.0	28	15	US-10-187-051-139	Sequence 139, App
815	3	10.0	28	15	US-10-187-051-141	Sequence 141, App
816	3	10.0	28	15	US-10-187-051-143	Sequence 143, App
817	3	10.0	28	15	US-10-187-051-145	Sequence 145, App
818	3	10.0	28	15	US-10-187-051-147	Sequence 147, App
819	3	10.0	28	15	US-10-187-051-149	Sequence 149, App
820	3	10.0	28	15	US-10-187-051-151	Sequence 151, App
821	3	10.0	28	15	US-10-187-051-155	Sequence 155, App
822	3	10.0	28	15	US-10-187-051-163	Sequence 163, App
823	3	10.0	28	15	US-10-187-051-165	Sequence 165, App
824	3	10.0	28	15	US-10-023-282-626	Sequence 626, App
825	3	10.0	28	15	US-10-023-282-638	Sequence 638, App
826	3	10.0	28	15	US-10-023-282-1089	Sequence 1089, Ap
827	3	10.0	28	15	US-10-255-532-6	Sequence 6, Appli
828	3	10.0	28	15	US-10-075-869-24	Sequence 24, Appl
829	3	10.0	28	15	US-10-202-724-3	Sequence 3, Appli
830	3	10.0	28	15	US-10-262-017-3	Sequence 3, Appli
831	3	10.0	28	15	US-10-106-698-5608	Sequence 5608, Ap
832	3	10.0	28	15	US-10-106-698-6764	Sequence 6764, Ap
833	3	10.0	28	15	US-10-106-698-7736	Sequence 7736, Ap
834	3	10.0	28	15	US-10-106-698-7875	Sequence 7875, Ap
835	3	10.0	28	15	US-10-106-698-8447	Sequence 8447, Ap
836	3	10.0	28	15	US-10-192-283A-12	Sequence 12, Appl
837	3	10.0	28	15	US-10-197-954-62	Sequence 62, Appl
838	3	10.0	28	15	US-10-197-954-145	Sequence 145, App
839	3	10.0	28	15	US-10-283-500-19	Sequence 19, Appl
840	3	10.0	28	15	US-10-295-981-19	Sequence 19, Appl
841	3	10.0	28	15	US-10-295-981-23	Sequence 23, Appl
842	3	10.0	28	15	US-10-160-290-22	Sequence 22, Appl
843	3	10.0	29	8	US-08-913-430-4	Sequence 4, Appli
844	3	10.0	29	9	US-09-205-658-71	Sequence 71, Appl
845	3	10.0	29	9	US-09-730-379B-4	Sequence 4, Appli
846	3	10.0	29	9	US-09-765-527-13	Sequence 13, Appl
847	3	10.0	29	9	US-09-765-527-64	Sequence 64, Appl
848	3	10.0	29	9	US-09-005-243-73	Sequence 73, Appl
849	3	10.0	29	9	US-09-904-380-23	Sequence 23, Appl
850	3	10.0	29	9	US-09-224-683-73	Sequence 73, Appl
851	3	10.0	29	9	US-09-932-161-1	Sequence 1, Appli
852	3	10.0	29	9	US-09-844-353A-71	Sequence 71, Appl
853	3	10.0	29	9	US-09-864-761-33834	Sequence 33834, A
854	3	10.0	29	9	US-09-864-761-34011	Sequence 34011, A

855	3	10.0	29	9	US-09-864-761-34337	Sequence 34337, A
856	3	10.0	29	9	US-09-864-761-35314	Sequence 35314, A
857	3	10.0	29	9	US-09-864-761-36235	Sequence 36235, A
858	3	10.0	29	9	US-09-864-761-37068	Sequence 37068, A
859	3	10.0	29	9	US-09-864-761-37579	Sequence 37579, A
860	3	10.0	29	9	US-09-864-761-37814	Sequence 37814, A
861	3	10.0	29	9	US-09-864-761-38222	Sequence 38222, A
862	3	10.0	29	9	US-09-864-761-38638	Sequence 38638, A
863	3	10.0	29	9	US-09-864-761-38968	Sequence 38968, A
864	3	10.0	29	9	US-09-864-761-39320	Sequence 39320, A
865	3	10.0	29	9	US-09-864-761-40067	Sequence 40067, A
866	3	10.0	29	9	US-09-864-761-40393	Sequence 40393, A
867	3	10.0	29	9	US-09-864-761-40727	Sequence 40727, A
868	3	10.0	29	9	US-09-864-761-40944	Sequence 40944, A
869	3	10.0	29	9	US-09-864-761-41199	Sequence 41199, A
870	3	10.0	29	9	US-09-864-761-41596	Sequence 41596, A
871	3	10.0	29	9	US-09-864-761-42035	Sequence 42035, A
872	3	10.0	29	9	US-09-864-761-42321	Sequence 42321, A
873	3	10.0	29	9	US-09-864-761-42342	Sequence 42342, A
874	3	10.0	29	9	US-09-864-761-42467	Sequence 42467, A
875	3	10.0	29	9	US-09-864-761-42588	Sequence 42588, A
876	3	10.0	29	9	US-09-864-761-42832	Sequence 42832, A
877	3	10.0	29	9	US-09-864-761-42924	Sequence 42924, A
878	3	10.0	29	9	US-09-864-761-43064	Sequence 43064, A
879	3	10.0	29	9	US-09-864-761-43635	Sequence 43635, A
880	3	10.0	29	9	US-09-864-761-44716	Sequence 44716, A
881	3	10.0	29	9	US-09-864-761-44947	Sequence 44947, A
882	3	10.0	29	9	US-09-864-761-45036	Sequence 45036, A
883	3	10.0	29	9	US-09-864-761-45207	Sequence 45207, A
884	3	10.0	29	9	US-09-864-761-45581	Sequence 45581, A
885	3	10.0	29	9	US-09-864-761-45777	Sequence 45777, A
886	3	10.0	29	9	US-09-864-761-45815	Sequence 45815, A
887	3	10.0	29	9	US-09-864-761-45948	Sequence 45948, A
888	3	10.0	29	9	US-09-864-761-46618	Sequence 46618, A
889	3	10.0	29	9	US-09-864-761-47028	Sequence 47028, A
890	3	10.0	29	9	US-09-864-761-47383	Sequence 47383, A
891	3	10.0	29	9	US-09-864-761-47524	Sequence 47524, A
892	3	10.0	29	9	US-09-864-761-48176	Sequence 48176, A
893	3	10.0	29	9	US-09-864-761-48505	Sequence 48505, A
894	3	10.0	29	9	US-09-864-761-48518	Sequence 48518, A
895	3	10.0	29	9	US-09-864-761-48746	Sequence 48746, A
896	3	10.0	29	9	US-09-876-388-22	Sequence 22, Appl
897	3	10.0	29	9	US-09-925-299-1270	Sequence 1270, Ap
898	3	10.0	29	9	US-09-764-869-638	Sequence 638, App
899	3	10.0	29	9	US-09-764-869-674	Sequence 674, App
900	3	10.0	29	9	US-09-881-490-3	Sequence 3, Appli
901	3	10.0	29	9	US-09-789-836-13	Sequence 13, Appl
902	3	10.0	29	10	US-09-927-112-5	Sequence 5, Appli
903	3	10.0	29	10	US-09-927-112-6	Sequence 6, Appli
904	3	10.0	29	10	US-09-872-864-17	Sequence 17, Appl
905	3	10.0	29	10	US-09-872-864-18	Sequence 18, Appl
906	3	10.0	29	10	US-09-872-864-19	Sequence 19, Appl
907	3	10.0	29	10	US-09-872-864-20	Sequence 20, Appl
908	3	10.0	29	10	US-09-922-261-258	Sequence 258, App
909	3	10.0	29	10	US-09-908-664-8	Sequence 8, Appli
910	3	10.0	29	10	US-09-908-664-9	Sequence 9, Appli
911	3	10.0	29	10	US-09-908-664-18	Sequence 18, Appl

912	3	10.0	29	10	US-09-905-831-12	Sequence 12, Appl
913	3	10.0	29	10	US-09-905-831-15	Sequence 15, Appl
914	3	10.0	29	10	US-09-003-869-79	Sequence 79, Appl
915	3	10.0	29	10	US-09-003-869-98	Sequence 98, Appl
916	3	10.0	29	10	US-09-911-969-7	Sequence 7, Appli
917	3	10.0	29	10	US-09-764-877-1395	Sequence 1395, Ap
918	3	10.0	29	10	US-09-867-852-152	Sequence 152, App
919	3	10.0	29	10	US-09-071-838-189	Sequence 189, App
920	3	10.0	29	10	US-09-071-838-242	Sequence 242, App
921	3	10.0	29	10	US-09-956-206A-1	Sequence 1, Appli
922	3	10.0	29	10	US-09-984-245-227	Sequence 227, App
923	3	10.0	29	11	US-09-956-940-38	Sequence 38, Appl
924	3	10.0	29	11	US-09-974-879-406	Sequence 406, App
925	3	10.0	29	11	US-09-974-879-511	Sequence 511, App
926	3	10.0	29	11	US-09-974-879-527	Sequence 527, App
927	3	10.0	29	11	US-09-974-879-580	Sequence 580, App
928	3	10.0	29	11	US-09-259-658-15	Sequence 15, Appl
929	3	10.0	29	11	US-09-756-690A-79	Sequence 79, Appl
930	3	10.0	29	11	US-09-756-690A-98	Sequence 98, Appl
931	3	10.0	29	11	US-09-843-221A-152	Sequence 152, App
932	3	10.0	29	11	US-09-925-299-1270	Sequence 1270, Ap
933	3	10.0	29	11	US-09-847-102A-80	Sequence 80, Appl
934	3	10.0	29	11	US-09-813-153-218	Sequence 218, App
935	3	10.0	29	11	US-09-966-262-227	Sequence 227, App
936	3	10.0	29	11	US-09-969-730-196	Sequence 196, App
937	3	10.0	29	11	US-09-983-966-227	Sequence 227, App
938	3	10.0	29	11	US-09-876-904A-28	Sequence 28, Appl
939	3	10.0	29	11	US-09-764-891-4191	Sequence 4191, Ap
940	3	10.0	29	11	US-09-764-891-4851	Sequence 4851, Ap
941	3	10.0	29	11	US-09-892-877-436	Sequence 436, App
942	3	10.0	29	11	US-09-847-208-125	Sequence 125, App
943	3	10.0	29	11	US-09-305-736-406	Sequence 406, App
944	3	10.0	29	11	US-09-305-736-512	Sequence 512, App
945	3	10.0	29	11	US-09-305-736-529	Sequence 529, App
946	3	10.0	29	11	US-09-305-736-581	Sequence 581, App
947	3	10.0	29	11	US-09-095-478-25	Sequence 25, Appl
948	3	10.0	29	11	US-09-908-139-19	Sequence 19, Appl
949	3	10.0	29	11	US-09-908-139-21	Sequence 21, Appl
950	3	10.0	29	11	US-09-491-614-14	Sequence 14, Appl
951	3	10.0	29	11	US-09-491-614-15	Sequence 15, Appl
952	3	10.0	29	11	US-09-948-783-438	Sequence 438, App
953	3	10.0	29	11	US-09-910-082A-158	Sequence 158, App
954	3	10.0	29	11	US-09-910-082A-368	Sequence 368, App
955	3	10.0	29	12	US-10-153-604A-72	Sequence 72, Appl
956	3	10.0	29	12	US-10-231-894-44	Sequence 44, Appl
957	3	10.0	29	12	US-10-234-816-95	Sequence 95, Appl
958	3	10.0	29	12	US-09-789-831-13	Sequence 13, Appl
959	3	10.0	29	12	US-09-935-384-757	Sequence 757, App
960	3	10.0	29	12	US-09-935-384-758	Sequence 758, App
961	3	10.0	29	12	US-10-131-909A-4	Sequence 4, Appli
962	3	10.0	29	12	US-10-131-909A-7	Sequence 7, Appli
963	3	10.0	29	12	US-10-096-777-1	Sequence 1, Appli
964	3	10.0	29	12	US-10-008-524A-123	Sequence 123, App
965	3	10.0	29	12	US-10-340-458-4	Sequence 4, Appli
966	3	10.0	29	12	US-10-340-458-21	Sequence 21, Appl
967	3	10.0	29	12	US-09-933-767-1182	Sequence 1182, Ap
968	3	10.0	29	12	US-09-963-693-71	Sequence 71, Appl

969	3	10.0	29	12	US-10-105-232-319	Sequence 319, App
970	3	10.0	29	12	US-10-105-232-512	Sequence 512, App
971	3	10.0	29	12	US-10-280-066-334	Sequence 334, App
972	3	10.0	29	12	US-10-289-135A-25	Sequence 25, Appl
973	3	10.0	29	12	US-10-029-386-27545	Sequence 27545, A
974	3	10.0	29	12	US-10-029-386-27995	Sequence 27995, A
975	3	10.0	29	12	US-10-029-386-29238	Sequence 29238, A
976	3	10.0	29	12	US-10-029-386-30063	Sequence 30063, A
977	3	10.0	29	12	US-10-029-386-30256	Sequence 30256, A
978	3	10.0	29	12	US-10-029-386-31071	Sequence 31071, A
979	3	10.0	29	12	US-10-029-386-31577	Sequence 31577, A
980	3	10.0	29	12	US-10-029-386-32473	Sequence 32473, A
981	3	10.0	29	12	US-10-029-386-33620	Sequence 33620, A
982	3	10.0	29	12	US-10-189-437-306	Sequence 306, App
983	3	10.0	29	12	US-10-189-437-499	Sequence 499, App
984	3	10.0	29	12	US-10-189-437-641	Sequence 641, App
985	3	10.0	29	12	US-10-189-437-693	Sequence 693, App
986	3	10.0	29	12	US-10-189-437-716	Sequence 716, App
987	3	10.0	29	12	US-10-231-889-44	Sequence 44, Appl
988	3	10.0	29	12	US-09-818-683-406	Sequence 406, App
989	3	10.0	29	12	US-09-818-683-512	Sequence 512, App
990	3	10.0	29	12	US-09-818-683-529	Sequence 529, App
991	3	10.0	29	12	US-09-818-683-581	Sequence 581, App
992	3	10.0	29	12	US-10-350-719-123	Sequence 123, App
993	3	10.0	29	12	US-09-933-780C-4	Sequence 4, Appli
994	3	10.0	29	12	US-10-074-024-284	Sequence 284, App
995	3	10.0	29	12	US-10-080-334-264	Sequence 264, App
996	3	10.0	29	12	US-10-154-884B-11109	Sequence 11109, A
997	3	10.0	29	12	US-10-227-577-638	Sequence 638, App
998	3	10.0	29	12	US-10-227-577-674	Sequence 674, App
999	3	10.0	29	12	US-10-264-049-3305	Sequence 3305, Ap
1000	3	10.0	29	12	US-10-387-977-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-843-221A-39

; Sequence 39, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-39

Query Match 100.0%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 2

US-09-843-221A-166

; Sequence 166, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

Query Match 100.0%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 3

US-09-169-786-2

; Sequence 2, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-169-786-2

Query Match 100.0%; Score 30; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 4

US-09-843-221A-27

; Sequence 27, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-843-221A-27

Query Match 100.0%; Score 30; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 5

US-09-843-221A-165

; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-165

Query Match 100.0%; Score 30; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 6

US-10-361-928-9

; Sequence 9, Application US/10361928
; Publication No. US20030144209A1

```
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Ser
US-10-361-928-9
```

```
Query Match          100.0%; Score 30; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
```

RESULT 7

```
US-09-169-786-3
; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-169-786-3
```

```
Query Match          100.0%; Score 30; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 8

US-09-928-047B-6

; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-6

Query Match 100.0%; Score 30; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 9

US-09-843-221A-16

; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-16

Query Match 100.0%; Score 30; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 10

US-09-843-221A-161

; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-161

Query Match 100.0%; Score 30; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 11

US-09-928-048A-6

; Sequence 6, Application US/09928048A
 ; Publication No. US20030138858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scantibodies Laboratory, Inc.
 ; APPLICANT: Cantor, Thomas L.
 ; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
 ; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
 ; FILE REFERENCE: 53221-20015.00
 ; CURRENT APPLICATION NUMBER: US/09/928,048A
 ; CURRENT FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-048A-6

Query Match 100.0%; Score 30; DB 12; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.2e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 12

US-10-361-928-8

; Sequence 8, Application US/10361928
 ; Publication No. US20030144209A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRINGHURST, F. RICHARD
 ; APPLICANT: TAKASU, HISASHI
 ; APPLICANT: GARDELLA, THOMAS J.
 ; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
 ; TITLE OF INVENTION: ANALOGS
 ; FILE REFERENCE: 0609.4630002
 ; CURRENT APPLICATION NUMBER: US/10/361,928
 ; CURRENT FILING DATE: 2003-02-11
 ; PRIOR APPLICATION NUMBER: 09/447,800
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: 60/110,152
 ; PRIOR FILING DATE: 1998-11-25
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: Desamino Ser

US-10-361-928-8

Query Match 100.0%; Score 30; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 13

US-10-340-484-15

; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 100.0%; Score 30; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 14

US-10-340-484-16

; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484

; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 100.0%; Score 30; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 15

US-10-016-403-5

; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

Query Match 100.0%; Score 30; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 16

US-10-097-079-1

; Sequence 1, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.

```

;      REGISTRATION NUMBER: 37,521
;      REFERENCE/DOCKET NUMBER: A2678B-WO
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (610) 454-2793
;      TELEFAX: (610) 454-3808
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 34 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: <Unknown>
;      TOPOLOGY: No. US20020132973A1 Relevant
;      MOLECULE TYPE: peptide
;      FRAGMENT TYPE: N-terminal
;      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-097-079-1

```

```

Query Match          100.0%;  Score 30;  DB 14;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 1.2e-23;
Matches   30;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

RESULT 17

US-10-168-185-9

```

; Sequence 9, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-9

```

```

Query Match          100.0%;  Score 30;  DB 12;  Length 37;
Best Local Similarity 100.0%;  Pred. No. 1.3e-23;
Matches   30;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||

```

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 18

US-09-169-786-4

; Sequence 4, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-4

Query Match 100.0%; Score 30; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 19

US-09-843-221A-14

; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUJK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT


```

; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-51

```

```

Query Match          96.7%; Score 29; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches    29; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

```

RESULT 22

```

US-09-843-221A-167
; Sequence 167, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 29
; TYPE: PRT

```


RESULT 24

US-10-361-928-3

```
; Sequence 3, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-10-361-928-3
```

```
Query Match          96.7%; Score 29; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        |||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
```

RESULT 25

US-10-361-928-6

```
; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
```

; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 96.7%; Score 29; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 26
US-09-843-221A-20
; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-20

Query Match 96.7%; Score 29; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 27

US-10-361-928-1

```
; Sequence 1, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
```

US-10-361-928-1

```
Query Match          96.7%; Score 29; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        |||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
```

RESULT 28

US-10-361-928-2

```
; Sequence 2, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-10-361-928-2

Query Match 96.7%; Score 29; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 29

US-10-361-928-5

; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-5

Query Match 96.7%; Score 29; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 30

US-09-843-221A-15

; Sequence 15, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-843-221A-15

Query Match 96.7%; Score 29; DB 11; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 29

RESULT 31

US-09-843-221A-52

; Sequence 52, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-52

Query Match 93.3%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 32

US-09-843-221A-168
; Sequence 168, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-168

Query Match 93.3%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 33

US-10-016-403-7

; Sequence 7, Application US/10016403

; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.

; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard

; STREET: 25 West Main Street

; CITY: Madison

; STATE: WI

; COUNTRY: USA

; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403

; FILING DATE: 10-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610

; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.

; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281

; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..34

; OTHER INFORMATION: /note= "modified parathyroid
; hormone"

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-016-403-7

Query Match 93.3%; Score 28; DB 14; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.3e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Db |||||
1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 34

US-10-372-095-24
; Sequence 24, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-095-24

Query Match 90.0%; Score 27; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQLMHNLGKHLNSMERVEWLRKKLQD 30
 |||||
Db 4 EIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 35

US-09-843-221A-50
; Sequence 50, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-50

Query Match 86.7%; Score 26; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 36

US-09-843-221A-28
; Sequence 28, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-28

Query Match 86.7%; Score 26; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 37

US-10-031-874A-206

; Sequence 206, Application US/10031874A
 ; Publication No. US20030190598A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANHA, JAMSHID
 ; APPLICANT: DUBUC, GINETTE
 ; APPLICANT: NARANG, SARAN
 ; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
 ; FILE REFERENCE: 11054-1
 ; CURRENT APPLICATION NUMBER: US/10/031,874A
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/207,234
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 206
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Lama glama
 US-10-031-874A-206

Query Match 86.7%; Score 26; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.3e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 38

US-09-843-221A-32

; Sequence 32, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 32
 ; LENGTH: 28
 ; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-843-221A-32

Query Match 80.0%; Score 24; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LMHNLGKHLNSMERVEWLRKKLQD 30
||||||||||||||||||||
Db 1 LMHNLGKHLNSMERVEWLRKKLQD 24

RESULT 39

US-10-016-403-6

; Sequence 6, Application US/10016403
; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-403-6

Query Match 80.0%; Score 24; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHNLGKHLNSMERVEWLRKKLQD 30
||||||||||||||||||||
Db 7 LMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 40

US-09-843-221A-124

; Sequence 124, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-124

Query Match 73.3%; Score 22; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVE 22
||||||||||||||||
Db 1 SVSEIQLMHNLGKHLNSMERVE 22

Search completed: January 14, 2004, 11:15:08
Job time : 21.1869 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 22.4299 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-166
Perfect score: 30
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	14	46.7	31	11	Q91Y90	Q91y90 peromyscus
2	14	46.7	31	11	Q91Y91	Q91y91 peromyscus
3	5	16.7	34	5	O17148	O17148 echinococcu
4	5	16.7	34	16	Q97K50	Q97k50 clostridium
5	5	16.7	34	17	Q9HR65	Q9hr65 halobacteri
6	5	16.7	35	11	Q8BTB9	Q8btb9 mus musculu
7	5	16.7	35	16	Q97RG6	Q97rg6 streptococc
8	4	13.3	28	10	O24285	O24285 pinus radia
9	4	13.3	28	10	Q8GZQ8	Q8gzq8 hordeum vul
10	4	13.3	29	2	Q49148	Q49148 methylobact
11	4	13.3	29	4	Q9UCL2	Q9ucl2 homo sapien
12	4	13.3	29	4	Q96PP3	Q96pp3 homo sapien
13	4	13.3	29	5	Q25603	Q25603 onchocerca
14	4	13.3	29	13	O13043	O13043 scyliorhinu
15	4	13.3	30	2	Q9JMV3	Q9jmv3 escherichia
16	4	13.3	30	4	Q9UBV5	Q9ubv5 homo sapien
17	4	13.3	30	16	Q8DZP7	Q8dzp7 streptococc
18	4	13.3	31	1	Q55314	Q55314 sulfolobus
19	4	13.3	31	4	Q8NEI8	Q8nei8 homo sapien
20	4	13.3	31	8	Q9MS77	Q9ms77 phacus acum
21	4	13.3	31	16	O50669	O50669 borrelia bu
22	4	13.3	32	11	Q9QZQ2	Q9qzq2 mus musculu
23	4	13.3	32	17	Q9HSZ0	Q9hsz0 halobacteri
24	4	13.3	33	5	Q95SD4	Q95sd4 drosophila
25	4	13.3	33	16	Q9PKX3	Q9pkx3 chlamydia m
26	4	13.3	34	2	Q9ZG81	Q9zq81 chlamydia t
27	4	13.3	34	2	Q8GFK2	Q8gfk2 staphylococ
28	4	13.3	34	11	Q8C4P4	Q8c4p4 mus musculu
29	4	13.3	34	13	Q90ZJ4	Q90zj4 gallus gall
30	4	13.3	34	16	Q98FK5	Q98fk5 rhizobium l
31	4	13.3	34	16	Q8G2Q2	Q8g2q2 brucella su
32	4	13.3	35	12	Q8V6J8	Q8v6j8 halovirus h
33	4	13.3	35	16	Q9KQG4	Q9kqg4 vibrio chol
34	4	13.3	35	16	Q8F102	Q8f102 leptospira
35	4	13.3	36	2	Q53920	Q53920 streptomyce
36	4	13.3	36	2	O68941	O68941 rhodospiril
37	4	13.3	36	4	Q8WXW8	Q8wxw8 homo sapien
38	4	13.3	36	10	Q9SJ63	Q9sj63 arabidopsis
39	4	13.3	36	12	Q9PXD1	Q9pxd1 hepatitis c
40	4	13.3	36	12	Q91D77	Q91d77 ttv-like mi
41	4	13.3	36	13	Q9YHT9	Q9yht9 brachydanio
42	4	13.3	36	16	Q97S91	Q97s91 streptococc
43	4	13.3	37	2	Q8KYJ0	Q8kyj0 bacillus an
44	4	13.3	37	5	Q9N2L2	Q9n2l2 caenorhabdi
45	4	13.3	37	10	Q39942	Q39942 helianthus
46	4	13.3	37	13	Q8Aww8	Q8aww8 oncorhynchu
47	4	13.3	37	16	Q8F6U2	Q8f6u2 leptospira
48	4	13.3	37	16	Q8F5H3	Q8f5h3 leptospira
49	4	13.3	37	16	Q8F419	Q8f419 leptospira
50	4	13.3	37	16	Q8EXV9	Q8exv9 leptospira
51	4	13.3	38	2	Q8KWH7	Q8kwh7 lactobacill
52	4	13.3	38	5	Q9NBE3	Q9nbe3 chironomus
53	4	13.3	38	5	Q9NBE5	Q9nbe5 chironomus
54	4	13.3	38	5	Q9NBE8	Q9nbe8 chironomus
55	4	13.3	38	5	Q9NBE4	Q9nbe4 chironomus
56	4	13.3	38	5	Q9NBE7	Q9nbe7 chironomus
57	4	13.3	38	11	Q91VC8	Q91vc8 mus musculu

58	4	13.3	38	13	Q8AWW9	Q8aww9 oncorhynchus
59	4	13.3	38	16	Q8E0D2	Q8e0d2 streptococcus
60	4	13.3	39	2	Q8GPO8	Q8gpo8 pseudomonas
61	4	13.3	39	10	Q9FEY1	Q9fey1 heterocapsa
62	4	13.3	39	12	Q68847	Q68847 hepatitis c
63	4	13.3	39	12	Q68845	Q68845 hepatitis c
64	4	13.3	39	12	Q68846	Q68846 hepatitis c
65	4	13.3	39	13	Q90776	Q90776 gallus gall
66	4	13.3	39	16	Q9KYH4	Q9kyh4 streptomyces
67	4	13.3	39	16	Q8F0C7	Q8f0c7 leptospira
68	4	13.3	39	16	Q8EZ33	Q8ez33 leptospira
69	4	13.3	40	2	Q8GCS7	Q8gcs7 eubacterium
70	4	13.3	40	4	P78340	P78340 homo sapiens
71	4	13.3	40	6	Q29283	Q29283 sus scrofa
72	4	13.3	40	10	Q8H192	Q8h192 arabidopsis
73	4	13.3	40	12	Q91JZ7	Q91jz7 hepatitis c
74	4	13.3	40	12	Q8V647	Q8v647 rabies virus
75	3	10.0	28	2	Q01303	Q01303 treponema p
76	3	10.0	28	2	Q05574	Q05574 prochloroth
77	3	10.0	28	2	Q9ZB83	Q9zb83 vibrio angu
78	3	10.0	28	3	Q8TGT8	Q8tgt8 saccharomyc
79	3	10.0	28	4	Q96SD9	Q96sd9 homo sapiens
80	3	10.0	28	4	Q16326	Q16326 homo sapiens
81	3	10.0	28	4	Q96EU0	Q96eu0 homo sapiens
82	3	10.0	28	4	O75980	O75980 homo sapiens
83	3	10.0	28	4	O95737	O95737 homo sapiens
84	3	10.0	28	5	Q8MUW0	Q8muw0 schistosoma
85	3	10.0	28	5	Q8MPY2	Q8mpy2 caenorhabdi
86	3	10.0	28	5	Q9BM68	Q9bm68 glottidia p
87	3	10.0	28	5	Q9BJE4	Q9bje4 pauropus sp
88	3	10.0	28	6	O62821	O62821 bubalus bub
89	3	10.0	28	6	Q9XS89	Q9xs89 equus caball
90	3	10.0	28	8	Q8WBC8	Q8wbc8 cucurbita e
91	3	10.0	28	8	Q9TIE9	Q9tie9 centella er
92	3	10.0	28	8	Q9TIE8	Q9tie8 centella as
93	3	10.0	28	8	Q9MR96	Q9mr96 crocodylus
94	3	10.0	28	8	Q9TIE6	Q9tie6 centella hi
95	3	10.0	28	8	Q9ZYS4	Q9zys4 leishmania
96	3	10.0	28	8	Q9MR94	Q9mr94 chelonia my
97	3	10.0	28	8	Q9TIE7	Q9tie7 centella tr
98	3	10.0	28	8	Q8HS23	Q8hs23 pisum sativ
99	3	10.0	28	8	Q8HS11	Q8hs11 spathiphyll
100	3	10.0	28	8	Q8HS07	Q8hs07 welwitschia
101	3	10.0	28	8	Q8HKF0	Q8hkf0 rhipicephal
102	3	10.0	28	9	Q9AZJ9	Q9azj9 bacteriophag
103	3	10.0	28	10	Q8S526	Q8s526 ipomoea bat
104	3	10.0	28	10	Q8W232	Q8w232 zeamays (m
105	3	10.0	28	10	Q944P1	Q944p1 manihot esc
106	3	10.0	28	11	Q9ESI4	Q9esi4 petromus ty
107	3	10.0	28	11	Q9ESI5	Q9esi5 thryonomys
108	3	10.0	28	11	Q9ESI6	Q9esi6 hystrix afr
109	3	10.0	28	11	Q99PL9	Q99pl9 mus musculus
110	3	10.0	28	11	Q9ESI2	Q9esi2 cryptomys h
111	3	10.0	28	11	Q9EP60	Q9ep60 heliophobiu
112	3	10.0	28	11	Q9ESI0	Q9esi0 cryptomys s
113	3	10.0	28	11	Q91XP0	Q91xp0 rattus norv
114	3	10.0	28	11	P70651	P70651 mus sp. bet

115	3	10.0	28	11	Q9EP59	Q9ep59 georychus c
116	3	10.0	28	11	Q9ESI1	Q9esi1 cryptomys d
117	3	10.0	28	11	P97914	P97914 rattus norv
118	3	10.0	28	11	Q9EP61	Q9ep61 heteroceph
119	3	10.0	28	11	Q9ESH8	Q9esh8 bathyergus
120	3	10.0	28	11	Q9ESH9	Q9esh9 bathyergus
121	3	10.0	28	11	Q9QXB4	Q9qxb4 mus musculu
122	3	10.0	28	11	Q9ESI3	Q9esi3 cryptomys h
123	3	10.0	28	12	Q67786	Q67786 human adeno
124	3	10.0	28	12	Q83181	Q83181 cauliflower
125	3	10.0	28	12	Q68552	Q68552 hepatitis c
126	3	10.0	28	12	Q9WNI4	Q9wni4 tt virus. o
127	3	10.0	28	13	Q9PRE8	Q9pre8 oryzias lat
128	3	10.0	28	13	Q9PRI9	Q9pri9 amia calva
129	3	10.0	28	13	Q9PRN8	Q9prn8 carassius a
130	3	10.0	28	15	O71346	O71346 human endog
131	3	10.0	28	15	Q9QEY3	Q9qey3 human immun
132	3	10.0	28	16	Q8X415	Q8x415 escherichia
133	3	10.0	28	16	Q8NVB8	Q8nvb8 staphylococ
134	3	10.0	28	16	Q8ENT7	Q8ent7 oceanobacil
135	3	10.0	28	16	Q8CK95	Q8ck95 yersinia pe
136	3	10.0	29	2	Q9ZGG4	Q9zgg4 heliobacill
137	3	10.0	29	2	Q54200	Q54200 streptomyce
138	3	10.0	29	2	Q9X3E3	Q9x3e3 prochloroco
139	3	10.0	29	2	Q9X3J9	Q9x3j9 prochloroco
140	3	10.0	29	2	Q47650	Q47650 escherichia
141	3	10.0	29	2	Q9AKV1	Q9akv1 neisseria g
142	3	10.0	29	2	Q9R526	Q9r526 vibrio chol
143	3	10.0	29	3	P78747	P78747 saccharomyc
144	3	10.0	29	3	Q8TGQ5	Q8tgq5 saccharomyc
145	3	10.0	29	4	Q9Y3G1	Q9y3g1 homo sapien
146	3	10.0	29	4	Q9H2A1	Q9h2a1 homo sapien
147	3	10.0	29	4	Q9UN87	Q9un87 homo sapien
148	3	10.0	29	4	Q9H465	Q9h465 homo sapien
149	3	10.0	29	4	Q8NEF6	Q8nef6 homo sapien
150	3	10.0	29	4	Q8TDW8	Q8tdw8 homo sapien
151	3	10.0	29	4	Q96IR5	Q96ir5 homo sapien
152	3	10.0	29	4	Q9BSQ3	Q9bsq3 homo sapien
153	3	10.0	29	5	Q95VB2	Q95vb2 spirometra
154	3	10.0	29	5	Q95NF4	Q95nf4 drosophila
155	3	10.0	29	5	Q8T936	Q8t936 folsomia ca
156	3	10.0	29	6	Q9TRG5	Q9trg5 sus scrofa
157	3	10.0	29	8	Q8WBB9	Q8wbb9 cucurbita f
158	3	10.0	29	8	Q8W7W7	Q8w7w7 cucurbita p
159	3	10.0	29	8	Q9GF70	Q9gf70 trochodendr
160	3	10.0	29	8	Q8W7W4	Q8w7w4 cucurbita a
161	3	10.0	29	8	Q8W7W6	Q8w7w6 cucurbita p
162	3	10.0	29	8	Q8WBC1	Q8wbc1 cucurbita o
163	3	10.0	29	8	Q9B5Z6	Q9b5z6 pseudostylo
164	3	10.0	29	8	Q8W7W5	Q8w7w5 cucurbita p
165	3	10.0	29	8	Q9B938	Q9b938 eupristina
166	3	10.0	29	8	Q9G370	Q9g370 draco blanf
167	3	10.0	29	8	Q8WBD0	Q8wbd0 cucurbita a
168	3	10.0	29	8	Q8WBB6	Q8wbb6 citrullus l
169	3	10.0	29	8	Q8W7W9	Q8w7w9 cucurbita f
170	3	10.0	29	8	Q8W7W8	Q8w7w8 cucurbita m
171	3	10.0	29	8	Q8HS21	Q8hs21 rheum x cul

172	3	10.0	29	9	Q9FZX6	Q9fzx6 bacterioph
173	3	10.0	29	10	P82196	P82196 spinacia ol
174	3	10.0	29	11	Q9Z2C0	Q9z2c0 mus musculu
175	3	10.0	29	11	Q921Z6	Q921z6 mus musculu
176	3	10.0	29	11	Q9Z2C1	Q9z2c1 mus musculu
177	3	10.0	29	11	070564	070564 mus musculu
178	3	10.0	29	11	Q9QY65	Q9qy65 mus musculu
179	3	10.0	29	11	Q62300	Q62300 mus musculu
180	3	10.0	29	11	008980	008980 mus musculu
181	3	10.0	29	11	Q8CGM8	Q8cgm8 mus musculu
182	3	10.0	29	12	Q91HB1	Q91hb1 porcine cir
183	3	10.0	29	12	092646	092646 hepatitis e
184	3	10.0	29	12	Q919A5	Q919a5 porcine rep
185	3	10.0	29	12	Q919A7	Q919a7 porcine rep
186	3	10.0	29	12	Q86872	Q86872 cauliflower
187	3	10.0	29	12	092648	092648 hepatitis e
188	3	10.0	29	12	056835	056835 vibrio chol
189	3	10.0	29	13	P82235	P82235 rana tempor
190	3	10.0	29	13	Q8AYR0	Q8ayr0 oryzias lat
191	3	10.0	29	13	Q8AWC2	Q8awc2 gallus gall
192	3	10.0	29	15	072001	072001 human endog
193	3	10.0	29	15	071342	071342 human endog
194	3	10.0	29	15	071339	071339 human endog
195	3	10.0	29	15	071347	071347 human endog
196	3	10.0	29	15	071340	071340 human endog
197	3	10.0	29	15	071343	071343 human endog
198	3	10.0	29	15	Q9IQJ8	Q9iqj8 human immun
199	3	10.0	29	15	071991	071991 human endog
200	3	10.0	29	15	Q9IQJ1	Q9iqj1 human immun
201	3	10.0	29	15	071994	071994 human endog
202	3	10.0	29	15	071341	071341 human endog
203	3	10.0	29	15	071345	071345 human endog
204	3	10.0	29	15	071336	071336 human endog
205	3	10.0	29	15	071344	071344 human endog
206	3	10.0	29	15	071338	071338 human endog
207	3	10.0	29	15	071992	071992 human endog
208	3	10.0	29	15	071337	071337 human endog
209	3	10.0	29	15	Q9IQJ9	Q9iqj9 human immun
210	3	10.0	29	15	071997	071997 human endog
211	3	10.0	29	15	071335	071335 human endog
212	3	10.0	29	16	Q9JZN6	Q9jzn6 neisseria m
213	3	10.0	29	16	Q8X419	Q8x419 escherichia
214	3	10.0	30	2	Q9JP75	Q9jp75 salmonella
215	3	10.0	30	2	Q9L8W9	Q9l8w9 streptomyce
216	3	10.0	30	2	Q9L8X1	Q9l8x1 streptomyce
217	3	10.0	30	2	Q9R4Z6	Q9r4z6 clostridium
218	3	10.0	30	2	Q9REI5	Q9rei5 acidiphiliu
219	3	10.0	30	2	Q9R4J2	Q9r4j2 helicobacte
220	3	10.0	30	2	Q8VUW9	Q8vuw9 staphylococ
221	3	10.0	30	2	Q9R4I5	Q9r4i5 mycoplasma
222	3	10.0	30	2	Q9R5Q3	Q9r5q3 leuconostoc
223	3	10.0	30	2	Q93GF6	Q93gf6 staphylococ
224	3	10.0	30	2	Q45966	Q45966 coxiella bu
225	3	10.0	30	2	Q9R5C4	Q9r5c4 comamonas.
226	3	10.0	30	2	Q9R5K3	Q9r5k3 leptospira
227	3	10.0	30	2	Q9R4I6	Q9r4i6 mycoplasma
228	3	10.0	30	2	Q9RER6	Q9rer6 enterobacte

229	3	10.0	30	3	Q8TGM3	Q8tgm3	saccharomyc
230	3	10.0	30	3	Q9URB0	Q9urb0	candida alb
231	3	10.0	30	3	Q8J172	Q8j172	trichoderma
232	3	10.0	30	3	Q8J171	Q8j171	hypocrea li
233	3	10.0	30	4	Q16330	Q16330	homo sapien
234	3	10.0	30	4	O95595	O95595	homo sapien
235	3	10.0	30	4	P78460	P78460	homo sapien
236	3	10.0	30	4	Q8N563	Q8n563	homo sapien
237	3	10.0	30	4	P78542	P78542	homo sapien
238	3	10.0	30	4	Q8IU66	Q8iu66	homo sapien
239	3	10.0	30	5	Q8SZJ6	Q8szj6	drosophila
240	3	10.0	30	5	Q9TWH7	Q9twh7	ancylostoma
241	3	10.0	30	5	Q968N1	Q968n1	tritrichomo
242	3	10.0	30	5	P82214	P82214	bombyx mori
243	3	10.0	30	6	Q9BDK1	Q9bdk1	bos taurus
244	3	10.0	30	6	Q9TTF9	Q9ttf9	ateles belz
245	3	10.0	30	8	Q8W7L1	Q8w7l1	cucurbita m
246	3	10.0	30	8	Q8W7K9	Q8w7k9	cucurbita p
247	3	10.0	30	8	Q8W7H8	Q8w7h8	cucurbita a
248	3	10.0	30	8	Q8WBC2	Q8wbc2	cucurbita o
249	3	10.0	30	8	Q8W7K8	Q8w7k8	cucurbita p
250	3	10.0	30	8	Q8W7H6	Q8w7h6	cucurbita m
251	3	10.0	30	8	Q8WBC4	Q8wbc4	cucurbita p
252	3	10.0	30	8	Q8W7L2	Q8w7l2	cucurbita a
253	3	10.0	30	8	Q8WBC6	Q8wbc6	cucurbita a
254	3	10.0	30	8	Q8WBB7	Q8wbb7	sechium edu
255	3	10.0	30	8	Q99328	Q99328	meloidogyne
256	3	10.0	30	8	Q8W7H7	Q8w7h7	cucurbita e
257	3	10.0	30	8	Q8WBC0	Q8wbc0	cucurbita f
258	3	10.0	30	8	Q9T2T8	Q9t2t8	bos taurus
259	3	10.0	30	8	Q8W7L0	Q8w7l0	cucurbita p
260	3	10.0	30	8	Q8HKG1	Q8hkg1	rhipicephal
261	3	10.0	30	9	Q8W674	Q8w674	enterobacte
262	3	10.0	30	10	Q9S8T2	Q9s8t2	cicer ariet
263	3	10.0	30	10	O23933	O23933	flaveria tr
264	3	10.0	30	10	Q8RUD1	Q8rud1	zea mays (m
265	3	10.0	30	10	Q93WY2	Q93wy2	oryza sativ
266	3	10.0	30	11	Q63885	Q63885	mus sp. cys
267	3	10.0	30	11	O88549	O88549	mesocricetu
268	3	10.0	30	11	Q8VDL1	Q8vdl1	mus musculu
269	3	10.0	30	11	Q9QV18	Q9qv18	rattus sp.
270	3	10.0	30	11	Q9QV14	Q9qv14	mus sp. col
271	3	10.0	30	11	Q9QV19	Q9qv19	rattus sp.
272	3	10.0	30	11	Q10753	Q10753	rattus norv
273	3	10.0	30	11	Q8BR32	Q8br32	mus musculu
274	3	10.0	30	12	Q91HB7	Q91hb7	tt virus. o
275	3	10.0	30	12	Q91HC4	Q91hc4	tt virus. o
276	3	10.0	30	12	Q9IJV5	Q9ijv5	norwalk vir
277	3	10.0	30	12	Q86870	Q86870	cauliflower
278	3	10.0	30	12	Q91HC3	Q91hc3	tt virus. o
279	3	10.0	30	12	Q9WLK3	Q9wlk3	hepatitis e
280	3	10.0	30	12	Q91HC0	Q91hc0	tt virus. o
281	3	10.0	30	13	O42551	O42551	brachydanio
282	3	10.0	30	13	Q9PRW0	Q9prw0	struthio ca
283	3	10.0	30	13	Q9PT00	Q9pt00	oncorhynchu
284	3	10.0	30	15	Q86599	Q86599	human endog
285	3	10.0	30	15	Q991P5	Q991p5	human immun

286	3	10.0	30	16	O50822	O50822 borrelia bu
287	3	10.0	30	16	Q9X0W9	Q9x0w9 thermotoga
288	3	10.0	30	16	Q9PP53	Q9pp53 campylobact
289	3	10.0	30	16	Q9KU55	Q9ku55 vibrio chol
290	3	10.0	30	16	Q9JWF4	Q9jwf4 neisseria m
291	3	10.0	30	16	Q97SX5	Q97sx5 streptococc
292	3	10.0	30	16	Q9K1W7	Q9klw7 chlamydia p
293	3	10.0	30	16	Q8U566	Q8u566 agrobacteri
294	3	10.0	30	16	Q8KE55	Q8ke55 chlorobium
295	3	10.0	30	16	Q93RS7	Q93rs7 streptomyce
296	3	10.0	30	16	Q8G1R1	Q8glr1 brucella su
297	3	10.0	30	16	Q8FZX9	Q8fzx9 brucella su
298	3	10.0	30	16	Q8CU88	Q8cu88 staphylococ
299	3	10.0	30	17	Q8ZZF0	Q8zzf0 pyrobaculum
300	3	10.0	30	17	Q8ZVL0	Q8zvl0 pyrobaculum
301	3	10.0	31	2	Q9S619	Q9s619 prochloroco
302	3	10.0	31	2	Q8KYK0	Q8kyk0 bacillus an
303	3	10.0	31	2	Q9JMV2	Q9jmv2 escherichia
304	3	10.0	31	2	Q9X3C3	Q9x3c3 prochloroco
305	3	10.0	31	2	O68825	O68825 pseudomonas
306	3	10.0	31	2	Q93GF7	Q93gf7 staphylococ
307	3	10.0	31	2	Q47323	Q47323 escherichia
308	3	10.0	31	2	Q9RHF9	Q9rhf9 acinetobact
309	3	10.0	31	2	Q9R4X1	Q9r4x1 treponema d
310	3	10.0	31	2	Q8KYI9	Q8kyi9 bacillus an
311	3	10.0	31	2	Q8RTS5	Q8rts5 uncultured
312	3	10.0	31	2	Q8L3D3	Q8l3d3 colwellia m
313	3	10.0	31	3	O94120	O94120 saccharomyc
314	3	10.0	31	4	Q96A45	Q96a45 homo sapien
315	3	10.0	31	4	Q9UHM9	Q9uhm9 homo sapien
316	3	10.0	31	4	Q9UEA9	Q9uea9 homo sapien
317	3	10.0	31	4	Q8WYF5	Q8wyf5 homo sapien
318	3	10.0	31	4	Q8N5X3	Q8n5x3 homo sapien
319	3	10.0	31	4	Q9BXM4	Q9bxm4 homo sapien
320	3	10.0	31	4	Q9UDE5	Q9ude5 homo sapien
321	3	10.0	31	5	Q8IQV3	Q8iqv3 drosophila
322	3	10.0	31	5	Q8IEY3	Q8iey3 trypanosoma
323	3	10.0	31	6	Q8MI94	Q8mi94 tupaia tana
324	3	10.0	31	6	Q9GLD6	Q9gld6 sus scrofa
325	3	10.0	31	6	Q8MIH5	Q8mih5 canis famil
326	3	10.0	31	6	O77625	O77625 bos taurus
327	3	10.0	31	6	Q8MIC3	Q8mic3 ochotona pr
328	3	10.0	31	6	Q95LC0	Q95lc0 sus scrofa
329	3	10.0	31	6	Q9N1C8	Q9n1c8 ovis aries
330	3	10.0	31	6	Q8MIC9	Q8mic9 nycticebus
331	3	10.0	31	6	Q9GKL4	Q9gkl4 canis famil
332	3	10.0	31	6	Q8MIG4	Q8mig4 cynocephalu
333	3	10.0	31	6	Q9XSB9	Q9xsb9 ateles belz
334	3	10.0	31	7	Q29868	Q29868 homo sapien
335	3	10.0	31	8	Q9MNM2	Q9mnm2 bufo americ
336	3	10.0	31	8	Q9MS59	Q9ms59 euglena san
337	3	10.0	31	8	O80011	O80011 enallagma a
338	3	10.0	31	8	Q9MS62	Q9ms62 euglena myx
339	3	10.0	31	8	Q34922	Q34922 limulus pol
340	3	10.0	31	8	Q8WEJ4	Q8wej4 gnetum gnem
341	3	10.0	31	8	Q9MS74	Q9ms74 euglena ana
342	3	10.0	31	8	Q9MS68	Q9ms68 euglena des

343	3	10.0	31	8	Q8M9Y3	Q8m9y3 chaetosphae
344	3	10.0	31	8	Q9MS53	Q9ms53 euglena vir
345	3	10.0	31	8	Q9MNL2	Q9mnl2 torrentophr
346	3	10.0	31	8	Q9MS56	Q9ms56 euglena ste
347	3	10.0	31	8	Q9MS78	Q9ms78 phacus acum
348	3	10.0	31	8	Q9MNL3	Q9mnl3 torrentophr
349	3	10.0	31	9	Q38499	Q38499 bacteriopha
350	3	10.0	31	10	Q9XIT0	Q9xit0 glycine max
351	3	10.0	31	10	Q8LKB4	Q8lkb4 musa acumin
352	3	10.0	31	11	Q8K1W2	Q8klw2 cavia porce
353	3	10.0	31	11	Q9QXB6	Q9qxb6 mus musculu
354	3	10.0	31	11	Q99KK6	Q99kk6 mus musculu
355	3	10.0	31	11	Q8K1P4	Q8klp4 sciurus vul
356	3	10.0	31	11	Q8CGM7	Q8cgm7 mus musculu
357	3	10.0	31	12	Q919E5	Q919e5 human papil
358	3	10.0	31	12	Q919E4	Q919e4 human papil
359	3	10.0	31	12	O56713	O56713 hepatitis c
360	3	10.0	31	12	Q919F7	Q919f7 human papil
361	3	10.0	31	12	Q919E6	Q919e6 human papil
362	3	10.0	31	12	O56692	O56692 hepatitis c
363	3	10.0	31	12	Q919F3	Q919f3 human papil
364	3	10.0	31	12	O56707	O56707 hepatitis c
365	3	10.0	31	12	O56687	O56687 hepatitis c
366	3	10.0	31	12	Q919F8	Q919f8 human papil
367	3	10.0	31	12	O56691	O56691 hepatitis c
368	3	10.0	31	12	Q919E1	Q919e1 human papil
369	3	10.0	31	12	O56701	O56701 hepatitis c
370	3	10.0	31	12	O56694	O56694 hepatitis c
371	3	10.0	31	12	Q919D9	Q919d9 human papil
372	3	10.0	31	12	Q919F6	Q919f6 human papil
373	3	10.0	31	12	Q919E3	Q919e3 human papil
374	3	10.0	31	12	O56712	O56712 hepatitis c
375	3	10.0	31	12	Q919E8	Q919e8 human papil
376	3	10.0	31	12	O56710	O56710 hepatitis c
377	3	10.0	31	12	O56688	O56688 hepatitis c
378	3	10.0	31	12	O56696	O56696 hepatitis c
379	3	10.0	31	12	O56695	O56695 hepatitis c
380	3	10.0	31	12	O56698	O56698 hepatitis c
381	3	10.0	31	12	O56702	O56702 hepatitis c
382	3	10.0	31	12	O56703	O56703 hepatitis c
383	3	10.0	31	12	O56697	O56697 hepatitis c
384	3	10.0	31	12	Q919F0	Q919f0 human papil
385	3	10.0	31	12	O56709	O56709 hepatitis c
386	3	10.0	31	12	Q919F4	Q919f4 human papil
387	3	10.0	31	12	O56689	O56689 hepatitis c
388	3	10.0	31	12	Q919F2	Q919f2 human papil
389	3	10.0	31	12	Q919F1	Q919f1 human papil
390	3	10.0	31	12	O56711	O56711 hepatitis c
391	3	10.0	31	12	Q919E2	Q919e2 human papil
392	3	10.0	31	12	Q919D8	Q919d8 human papil
393	3	10.0	31	12	O56686	O56686 hepatitis c
394	3	10.0	31	12	Q9WMX5	Q9wmx5 human echov
395	3	10.0	31	12	O56690	O56690 hepatitis c
396	3	10.0	31	12	Q919E9	Q919e9 human papil
397	3	10.0	31	12	O56706	O56706 hepatitis c
398	3	10.0	31	12	O56700	O56700 hepatitis c
399	3	10.0	31	12	O56704	O56704 hepatitis c

400	3	10.0	31	12	Q919D7	Q919d7 human papil
401	3	10.0	31	12	Q919F5	Q919f5 human papil
402	3	10.0	31	12	056693	056693 hepatitis c
403	3	10.0	31	12	056685	056685 hepatitis c
404	3	10.0	31	12	056708	056708 hepatitis c
405	3	10.0	31	12	Q919E0	Q919e0 human papil
406	3	10.0	31	12	056705	056705 hepatitis c
407	3	10.0	31	12	Q919E7	Q919e7 human papil
408	3	10.0	31	12	Q914M9	Q914m9 sulfolobus
409	3	10.0	31	12	056699	056699 hepatitis c
410	3	10.0	31	13	042540	042540 brachydanio
411	3	10.0	31	13	Q91763	Q91763 xenopus lae
412	3	10.0	31	13	Q9PSU1	Q9psu1 xenopus lae
413	3	10.0	31	13	Q91816	Q91816 xenopus lae
414	3	10.0	31	15	Q83937	Q83937 ovine lenti
415	3	10.0	31	16	025108	025108 helicobacte
416	3	10.0	31	16	050709	050709 borrelia bu
417	3	10.0	31	16	050858	050858 borrelia bu
418	3	10.0	31	16	051007	051007 borrelia bu
419	3	10.0	31	16	Q9PGF2	Q9pgf2 xylella fas
420	3	10.0	31	16	Q9PAW4	Q9paw4 xylella fas
421	3	10.0	31	16	Q9KVF3	Q9kvf3 vibrio chol
422	3	10.0	31	16	Q97SZ9	Q97sz9 streptococc
423	3	10.0	31	16	Q97SW8	Q97sw8 streptococc
424	3	10.0	31	16	Q97QJ4	Q97qj4 streptococc
425	3	10.0	31	16	Q97QB7	Q97qb7 streptococc
426	3	10.0	31	16	Q97CV6	Q97cv6 streptococc
427	3	10.0	31	16	Q9K2A0	Q9k2a0 chlamydia p
428	3	10.0	31	16	Q9K236	Q9k236 chlamydia p
429	3	10.0	31	16	Q8P9W1	Q8p9w1 xanthomonas
430	3	10.0	31	16	Q8KEV8	Q8kev8 chlorobium
431	3	10.0	31	16	Q8KCQ0	Q8kcq0 chlorobium
432	3	10.0	31	16	Q8KBJ8	Q8kbj8 chlorobium
433	3	10.0	31	16	Q8EIW8	Q8eiw8 shewanella
434	3	10.0	31	16	Q8EI77	Q8ei77 shewanella
435	3	10.0	31	16	Q8E9Y5	Q8e9y5 shewanella
436	3	10.0	31	16	Q8E8G1	Q8e8g1 shewanella
437	3	10.0	31	16	Q8CTA2	Q8cta2 staphylococ
438	3	10.0	32	2	Q9AJ41	Q9aj41 buchnera ap
439	3	10.0	32	2	Q00491	Q00491 streptomyce
440	3	10.0	32	2	Q49249	Q49249 mycoplasma
441	3	10.0	32	2	Q44499	Q44499 anabaena va
442	3	10.0	32	2	Q9S629	Q9s629 prochloroco
443	3	10.0	32	2	Q8KYN3	Q8kyn3 bacillus an
444	3	10.0	32	2	Q44509	Q44509 azotobacter
445	3	10.0	32	2	Q45534	Q45534 bacillus su
446	3	10.0	32	2	Q8VN21	Q8vn21 kluyvera ci
447	3	10.0	32	2	Q9R5Q7	Q9r5q7 aeromonas h
448	3	10.0	32	2	Q8KYM4	Q8kym4 bacillus an
449	3	10.0	32	2	032493	032493 bacteroides
450	3	10.0	32	2	Q8VNT6	Q8vnt6 enterobacte
451	3	10.0	32	2	Q9L373	Q9l373 rhizobium l
452	3	10.0	32	2	Q8GF58	Q8gf58 zymomonas m
453	3	10.0	32	3	Q01058	Q01058 kluyveromyc
454	3	10.0	32	3	Q8TGT3	Q8tgt3 saccharomyc
455	3	10.0	32	4	Q12900	Q12900 homo sapien
456	3	10.0	32	4	Q9UEB0	Q9ueb0 homo sapien

457	3	10.0	32	4	Q8TC25	Q8tc25	homo sapien
458	3	10.0	32	4	Q96GM7	Q96gm7	homo sapien
459	3	10.0	32	4	Q9HAX8	Q9hax8	homo sapien
460	3	10.0	32	4	Q8TBQ3	Q8tbq3	homo sapien
461	3	10.0	32	4	Q96I20	Q96i20	homo sapien
462	3	10.0	32	4	Q9UN69	Q9un69	homo sapien
463	3	10.0	32	4	Q9UQV1	Q9uqv1	homo sapien
464	3	10.0	32	5	Q9GPD9	Q9gpd9	drosophila
465	3	10.0	32	5	Q8T382	Q8t382	leishmania
466	3	10.0	32	5	O96634	O96634	trypanosoma
467	3	10.0	32	5	Q9TWR8	Q9twr8	procambarus
468	3	10.0	32	5	O18606	O18606	branchiosto
469	3	10.0	32	5	Q8T757	Q8t757	branchiosto
470	3	10.0	32	6	Q9TR67	Q9tr67	sus scrofa
471	3	10.0	32	6	Q8MJ91	Q8mj91	macaca mula
472	3	10.0	32	7	Q8SNF1	Q8snf1	gallinago m
473	3	10.0	32	7	O19722	O19722	homo sapien
474	3	10.0	32	8	Q36494	Q36494	farfantepen
475	3	10.0	32	8	Q8SL89	Q8sl89	euglena ste
476	3	10.0	32	8	Q9GF95	Q9gf95	cercidiphyl
477	3	10.0	32	8	Q31736	Q31736	beta vulgar
478	3	10.0	32	8	Q8SL87	Q8sl87	euglena vir
479	3	10.0	32	8	Q31735	Q31735	beta vulgar
480	3	10.0	32	8	Q9MNM0	Q9nmn0	bufo andrew
481	3	10.0	32	8	Q9MNL0	Q9mnl0	bufo danate
482	3	10.0	32	8	Q951Q4	Q951q4	renilla ren
483	3	10.0	32	8	Q9GF72	Q9gf72	saururus ce
484	3	10.0	32	9	Q9MBU5	Q9mbu5	chlamydia p
485	3	10.0	32	10	Q8S527	Q8s527	ipomoea bat
486	3	10.0	32	10	Q8RXQ5	Q8rxq5	arabidopsis
487	3	10.0	32	10	Q40727	Q40727	oryza sativ
488	3	10.0	32	11	Q9JIU1	Q9jiu1	rattus norv
489	3	10.0	32	11	Q9ROE3	Q9r0e3	mus musculu
490	3	10.0	32	11	Q9QWM2	Q9qwm2	mus musculu
491	3	10.0	32	11	Q9QWB2	Q9qwb2	rattus sp.
492	3	10.0	32	11	Q9QXX1	Q9qxx1	mus musculu
493	3	10.0	32	11	Q8C2N8	Q8c2n8	mus musculu
494	3	10.0	32	11	Q8BS12	Q8bs12	mus musculu
495	3	10.0	32	12	Q9PXV2	Q9pxv2	hepatitis b
496	3	10.0	32	12	Q9WNI5	Q9wni5	tt virus. o
497	3	10.0	32	12	Q914F9	Q914f9	sulfolobus
498	3	10.0	32	12	Q8QYT4	Q8qyt4	grapevine v
499	3	10.0	32	12	Q8QYT7	Q8qyt7	grapevine v
500	3	10.0	32	12	Q8QYU0	Q8qyu0	grapevine v
501	3	10.0	32	12	Q9Q934	Q9q934	shope fibro
502	3	10.0	32	13	Q8QG73	Q8qg73	oncorhynchu
503	3	10.0	32	13	Q8QG72	Q8qg72	salmo salar
504	3	10.0	32	13	Q8QG71	Q8qg71	oncorhynchu
505	3	10.0	32	13	Q9PS21	Q9ps21	carassius a
506	3	10.0	32	13	Q8QG84	Q8qg84	oncorhynchu
507	3	10.0	32	13	Q8QG83	Q8qg83	oncorhynchu
508	3	10.0	32	13	Q8QG82	Q8qg82	oncorhynchu
509	3	10.0	32	13	Q8QG70	Q8qg70	salvelinus
510	3	10.0	32	13	P82780	P82780	rana catesb
511	3	10.0	32	13	Q9W7P3	Q9w7p3	morone saxa
512	3	10.0	32	13	Q9W7P2	Q9w7p2	morone saxa
513	3	10.0	32	16	O50706	O50706	borrelia bu

514	3	10.0	32	16	O50851	O50851 borrelia bu
515	3	10.0	32	16	O50865	O50865 borrelia bu
516	3	10.0	32	16	O51003	O51003 borrelia bu
517	3	10.0	32	16	Q9PGT0	Q9pgt0 xylella fas
518	3	10.0	32	16	Q9KTV2	Q9ktv2 vibrio chol
519	3	10.0	32	16	Q9KPN9	Q9kpn9 vibrio chol
520	3	10.0	32	16	Q9KLF0	Q9klf0 vibrio chol
521	3	10.0	32	16	Q9K7B0	Q9k7b0 bacillus ha
522	3	10.0	32	16	Q9A2H0	Q9a2h0 caulobacter
523	3	10.0	32	16	Q98AB6	Q98ab6 rhizobium l
524	3	10.0	32	16	Q8X3V6	Q8x3v6 escherichia
525	3	10.0	32	16	Q8KG49	Q8kg49 chlorobium
526	3	10.0	32	16	Q8KEZ9	Q8kez9 chlorobium
527	3	10.0	32	16	Q8KCV3	Q8kcv3 chlorobium
528	3	10.0	32	16	Q9K4G0	Q9k4g0 streptomyce
529	3	10.0	32	16	Q8EAD5	Q8ead5 shewanella
530	3	10.0	32	16	Q8CU60	Q8cu60 staphylococ
531	3	10.0	32	16	Q8CTR7	Q8ctr7 staphylococ
532	3	10.0	32	16	Q8CRE7	Q8cre7 staphylococ
533	3	10.0	32	17	Q8ZZF7	Q8zzf7 pyrobaculum
534	3	10.0	33	1	Q9UWL4	Q9uwl4 methanopyru
535	3	10.0	33	2	Q8KH96	Q8kh96 pseudomonas
536	3	10.0	33	2	Q9S624	Q9s624 prochloroco
537	3	10.0	33	2	Q9R2M3	Q9r2m3 prochloroco
538	3	10.0	33	2	Q9X3M5	Q9x3m5 prochloroco
539	3	10.0	33	2	Q9S651	Q9s651 streptococc
540	3	10.0	33	2	Q9K370	Q9k370 rhizobium l
541	3	10.0	33	2	Q9S3N5	Q9s3n5 bacillus ce
542	3	10.0	33	2	Q8KQ80	Q8kq80 vibrio chol
543	3	10.0	33	2	Q56414	Q56414 escherichia
544	3	10.0	33	2	Q9S622	Q9s622 prochloroco
545	3	10.0	33	2	Q9K2V1	Q9k2v1 rhizobium l
546	3	10.0	33	2	Q9F1F4	Q9f1f4 enterococcu
547	3	10.0	33	2	Q9KI23	Q9ki23 helicobacte
548	3	10.0	33	2	Q8GQU2	Q8gqu2 leptospira
549	3	10.0	33	3	Q8TGR1	Q8tgr1 saccharomyc
550	3	10.0	33	4	Q99950	Q99950 homo sapien
551	3	10.0	33	4	Q9UP36	Q9up36 homo sapien
552	3	10.0	33	4	Q15285	Q15285 homo sapien
553	3	10.0	33	4	Q9UDI1	Q9udi1 homo sapien
554	3	10.0	33	4	Q9P1T8	Q9plt8 homo sapien
555	3	10.0	33	4	Q9BV16	Q9bvl6 homo sapien
556	3	10.0	33	4	Q92668	Q92668 homo sapien
557	3	10.0	33	5	Q9GTB2	Q9gtb2 eimeria ten
558	3	10.0	33	5	Q9GT93	Q9gt93 cryptospori
559	3	10.0	33	5	Q26673	Q26673 tethya aura
560	3	10.0	33	5	Q26672	Q26672 tethya aura
561	3	10.0	33	5	Q9GTC2	Q9gtc2 plasmodium
562	3	10.0	33	5	Q27637	Q27637 drosophila
563	3	10.0	33	5	Q9GTB3	Q9gtb3 eimeria ten
564	3	10.0	33	5	Q9GTA6	Q9gta6 sarcocystis
565	3	10.0	33	5	Q9GTA1	Q9gta1 babesia bov
566	3	10.0	33	5	Q17293	Q17293 cancer ante
567	3	10.0	33	5	Q27310	Q27310 paramecium
568	3	10.0	33	5	Q9GTA9	Q9gta9 sarcocystis
569	3	10.0	33	5	O17147	O17147 echinococcu
570	3	10.0	33	5	Q9GT95	Q9gt95 cryptospori

571	3	10.0	33	5	Q9GTA2	Q9gta2 babesia bov
572	3	10.0	33	6	Q28788	Q28788 papio hamad
573	3	10.0	33	6	O18916	O18916 sus scrofa
574	3	10.0	33	6	Q9TSX7	Q9tsx7 sus scrofa
575	3	10.0	33	6	Q95M05	Q95m05 bos taurus
576	3	10.0	33	7	Q8MGU2	Q8mgu2 bos taurus
577	3	10.0	33	7	Q8SNF0	Q8snf0 gallinago m
578	3	10.0	33	8	Q9BAC6	Q9bac6 euglena gra
579	3	10.0	33	8	Q8W9G0	Q8w9g0 meloidogyne
580	3	10.0	33	8	Q9BAC1	Q9bac1 euglena ste
581	3	10.0	33	8	Q9XNP3	Q9xnp3 boophilus m
582	3	10.0	33	8	O78857	O78857 phytophthor
583	3	10.0	33	8	Q9T2N1	Q9t2n1 nicotiana t
584	3	10.0	33	8	Q9BAC4	Q9bac4 euglena mut
585	3	10.0	33	8	Q8WEJ5	Q8wej5 ginkgo bilo
586	3	10.0	33	8	Q8HUH3	Q8huh3 chlamydomon
587	3	10.0	33	8	Q8HS33	Q8hs33 hydrastis c
588	3	10.0	33	9	Q38588	Q38588 bacteriopha
589	3	10.0	33	9	Q38551	Q38551 bacteriopha
590	3	10.0	33	10	O49775	O49775 arabidopsis
591	3	10.0	33	10	Q9S8V5	Q9s8v5 zea mays (m
592	3	10.0	33	10	Q9AYQ5	Q9ayq5 cucumis sat
593	3	10.0	33	11	Q9QVM2	Q9qvm2 mus sp. glu
594	3	10.0	33	12	O72982	O72982 hepatitis c
595	3	10.0	33	12	O73068	O73068 hepatitis c
596	3	10.0	33	12	Q90085	Q90085 human papil
597	3	10.0	33	12	O72979	O72979 hepatitis c
598	3	10.0	33	12	Q91J04	Q91j04 tt virus. o
599	3	10.0	33	12	O72996	O72996 hepatitis c
600	3	10.0	33	12	Q91J14	Q91j14 tt virus. o
601	3	10.0	33	12	O72988	O72988 hepatitis c
602	3	10.0	33	12	O72992	O72992 hepatitis c
603	3	10.0	33	12	Q91J12	Q91j12 tt virus. o
604	3	10.0	33	12	Q91J15	Q91j15 tt virus. o
605	3	10.0	33	12	Q91J07	Q91j07 tt virus. o
606	3	10.0	33	12	O72995	O72995 hepatitis c
607	3	10.0	33	12	Q91J09	Q91j09 tt virus. o
608	3	10.0	33	12	O72990	O72990 hepatitis c
609	3	10.0	33	12	O73010	O73010 hepatitis c
610	3	10.0	33	12	Q86912	Q86912 hepatitis c
611	3	10.0	33	12	Q8V5G7	Q8v5g7 hepatitis c
612	3	10.0	33	12	O72981	O72981 hepatitis c
613	3	10.0	33	12	Q91J08	Q91j08 tt virus. o
614	3	10.0	33	12	O72997	O72997 hepatitis c
615	3	10.0	33	12	O73008	O73008 hepatitis c
616	3	10.0	33	12	Q83963	Q83963 avian influ
617	3	10.0	33	12	O72986	O72986 hepatitis c
618	3	10.0	33	12	O72993	O72993 hepatitis c
619	3	10.0	33	12	Q91J06	Q91j06 tt virus. o
620	3	10.0	33	12	O72984	O72984 hepatitis c
621	3	10.0	33	12	O73005	O73005 hepatitis c
622	3	10.0	33	12	O73067	O73067 hepatitis c
623	3	10.0	33	12	O72985	O72985 hepatitis c
624	3	10.0	33	12	O72999	O72999 hepatitis c
625	3	10.0	33	12	Q91J16	Q91j16 tt virus. o
626	3	10.0	33	12	O72998	O72998 hepatitis c
627	3	10.0	33	12	Q91J11	Q91j11 tt virus. o

628	3	10.0	33	12	072994	072994 hepatitis c
629	3	10.0	33	12	Q8V5H0	Q8v5h0 hepatitis c
630	3	10.0	33	12	Q91J13	Q91j13 tt virus. o
631	3	10.0	33	12	Q8V5G8	Q8v5g8 hepatitis c
632	3	10.0	33	12	072983	072983 hepatitis c
633	3	10.0	33	12	073007	073007 hepatitis c
634	3	10.0	33	12	Q91J10	Q91j10 tt virus. o
635	3	10.0	33	12	072987	072987 hepatitis c
636	3	10.0	33	12	Q91J17	Q91j17 tt virus. o
637	3	10.0	33	12	Q69461	Q69461 human herpe
638	3	10.0	33	12	Q8V5G9	Q8v5g9 hepatitis c
639	3	10.0	33	12	072978	072978 hepatitis c
640	3	10.0	33	12	073009	073009 hepatitis c
641	3	10.0	33	12	073004	073004 hepatitis c
642	3	10.0	33	12	Q99138	Q99138 avian influ
643	3	10.0	33	13	P82740	P82740 rana tempor
644	3	10.0	33	13	P82236	P82236 rana tempor
645	3	10.0	33	15	Q9DZ98	Q9dz98 human immun
646	3	10.0	33	15	Q86107	Q86107 simian sarc
647	3	10.0	33	16	Q9PA23	Q9pa23 xylella fas
648	3	10.0	33	16	Q9KQP4	Q9kqp4 vibrio chol
649	3	10.0	33	16	Q9KML1	Q9kml1 vibrio chol
650	3	10.0	33	16	Q97T91	Q97t91 streptococc
651	3	10.0	33	16	Q97PC1	Q97pc1 streptococc
652	3	10.0	33	16	Q932N2	Q932n2 staphylococ
653	3	10.0	33	16	Q8ZKL2	Q8zkl2 salmonella
654	3	10.0	33	16	Q8Z1V4	Q8z1v4 salmonella
655	3	10.0	33	16	Q8U5M4	Q8u5m4 agrobacteri
656	3	10.0	33	16	Q8VK01	Q8vk01 mycobacteri
657	3	10.0	33	16	Q8NUL1	Q8nul1 staphylococ
658	3	10.0	33	16	Q8NT95	Q8nt95 corynebacte
659	3	10.0	33	16	Q8NLP2	Q8nlp2 corynebacte
660	3	10.0	33	16	Q8KG99	Q8kg99 chlorobium
661	3	10.0	33	16	Q8KBZ0	Q8kbz0 chlorobium
662	3	10.0	33	16	Q8G0U8	Q8g0u8 brucella su
663	3	10.0	33	16	Q8FZ67	Q8fz67 brucella su
664	3	10.0	33	16	Q8FYR6	Q8fyr6 brucella su
665	3	10.0	33	16	Q8FY86	Q8fy86 brucella su
666	3	10.0	33	16	Q8FSG0	Q8fsg0 corynebacte
667	3	10.0	33	16	Q8EJH6	Q8ejh6 shewanella
668	3	10.0	33	16	Q8EGA9	Q8ega9 shewanella
669	3	10.0	33	16	Q8EE59	Q8ee59 shewanella
670	3	10.0	33	16	Q8EE42	Q8ee42 shewanella
671	3	10.0	33	16	Q8E8W4	Q8e8w4 shewanella
672	3	10.0	33	16	Q8E1Y5	Q8ely5 streptococc
673	3	10.0	33	16	Q8CTR8	Q8ctr8 staphylococ
674	3	10.0	33	16	Q8CQY7	Q8cqy7 staphylococ
675	3	10.0	33	17	Q9HSX6	Q9hsx6 halobacteri
676	3	10.0	33	17	Q8U2X8	Q8u2x8 pyrococcus
677	3	10.0	34	2	Q54427	Q54427 spiroplasma
678	3	10.0	34	2	Q9X3L6	Q9x3l6 prochloroco
679	3	10.0	34	2	Q9R5U1	Q9r5u1 campylobact
680	3	10.0	34	2	Q44208	Q44208 pseudomonas
681	3	10.0	34	2	Q9X7J6	Q9x7j6 pseudomonas
682	3	10.0	34	2	Q8KYH2	Q8kyh2 bacillus an
683	3	10.0	34	2	O31061	O31061 butyrivibri
684	3	10.0	34	2	Q9R8A2	Q9r8a2 chlamydia t

685	3	10.0	34	2	Q9RZW6	Q9rzw6 borrelia bu
686	3	10.0	34	2	Q8GJC8	Q8gjc8 campylobact
687	3	10.0	34	2	Q8G8C9	Q8g8c9 pseudomonas
688	3	10.0	34	3	Q00377	Q00377 coccidioide
689	3	10.0	34	4	Q99910	Q99910 homo sapien
690	3	10.0	34	4	Q9H3R8	Q9h3r8 homo sapien
691	3	10.0	34	4	Q9UI64	Q9ui64 homo sapien
692	3	10.0	34	4	Q8WY57	Q8wy57 homo sapien
693	3	10.0	34	4	Q8WW51	Q8ww51 homo sapien
694	3	10.0	34	4	Q9BSP7	Q9bsp7 homo sapien
695	3	10.0	34	4	Q9H4L8	Q9h4l8 homo sapien
696	3	10.0	34	4	Q8NEQ3	Q8neq3 homo sapien
697	3	10.0	34	4	Q15251	Q15251 homo sapien
698	3	10.0	34	4	Q9NQY9	Q9nqy9 homo sapien
699	3	10.0	34	5	Q9BIP7	Q9bip7 cooperia pu
700	3	10.0	34	5	Q27821	Q27821 trichomonas
701	3	10.0	34	5	Q9GQE5	Q9gqe5 branchiosto
702	3	10.0	34	6	Q9TS91	Q9ts91 oryctolagus
703	3	10.0	34	6	P79429	P79429 capra hircu
704	3	10.0	34	6	Q9TRI2	Q9tri2 sus scrofa
705	3	10.0	34	6	P82908	P82908 bos taurus
706	3	10.0	34	8	O79025	O79025 enallagma v
707	3	10.0	34	8	Q9T2T7	Q9t2t7 bos taurus
708	3	10.0	34	8	Q8MCA2	Q8mca2 phaseolus a
709	3	10.0	34	8	Q8HKE1	Q8hke1 rhipicephal
710	3	10.0	34	10	Q8W2H0	Q8w2h0 paspalum no
711	3	10.0	34	10	Q8VWL0	Q8vwl0 paspalum no
712	3	10.0	34	10	Q9SCA3	Q9sca3 lycopersico
713	3	10.0	34	11	Q923Z1	Q923z1 mus musculu
714	3	10.0	34	11	Q8R557	Q8r557 mus musculu
715	3	10.0	34	11	Q9ET72	Q9et72 mus musculu
716	3	10.0	34	11	Q99KM9	Q99km9 mus musculu
717	3	10.0	34	11	Q99KX7	Q99kx7 mus musculu
718	3	10.0	34	11	Q64170	Q64170 mus sp. b-r
719	3	10.0	34	11	Q8VHL4	Q8vhl4 rattus norv
720	3	10.0	34	12	Q9DW68	Q9dw68 rat cytomeg
721	3	10.0	34	13	O42521	O42521 scyliorhinu
722	3	10.0	34	13	O13101	O13101 ambystoma m
723	3	10.0	34	13	Q8QGG2	Q8qgg2 oncorhynchu
724	3	10.0	34	13	Q8QFM9	Q8qfm9 oncorhynchu
725	3	10.0	34	13	O42526	O42526 scyliorhinu
726	3	10.0	34	13	Q9PRE7	Q9pre7 oryzias lat
727	3	10.0	34	13	Q8QGG1	Q8qgg1 oncorhynchu
728	3	10.0	34	13	Q8QGF7	Q8qgf7 oncorhynchu
729	3	10.0	34	13	Q98TM8	Q98tm8 platichthys
730	3	10.0	34	15	O40445	O40445 human immun
731	3	10.0	34	15	Q9WR32	Q9wr32 human immun
732	3	10.0	34	15	Q9W8Y1	Q9w8y1 chimpanzee
733	3	10.0	34	16	O50812	O50812 borrelia bu
734	3	10.0	34	16	O50877	O50877 borrelia bu
735	3	10.0	34	16	Q9PGH3	Q9pgh3 xylella fas
736	3	10.0	34	16	Q9PGF8	Q9pgf8 xylella fas
737	3	10.0	34	16	Q9PDD0	Q9pdd0 xylella fas
738	3	10.0	34	16	Q9KRA8	Q9kra8 vibrio chol
739	3	10.0	34	16	Q9KPW9	Q9kpw9 vibrio chol
740	3	10.0	34	16	Q9KM63	Q9km63 vibrio chol
741	3	10.0	34	16	Q9K7C6	Q9k7c6 bacillus ha

742	3	10.0	34	16	Q9JY24	Q9jy24 neisseria m
743	3	10.0	34	16	Q9JVP3	Q9jvp3 neisseria m
744	3	10.0	34	16	Q9JUR9	Q9jur9 neisseria m
745	3	10.0	34	16	Q97SF7	Q97sf7 streptococc
746	3	10.0	34	16	Q97PI6	Q97pi6 streptococc
747	3	10.0	34	16	Q9K2B9	Q9k2b9 chlamydia p
748	3	10.0	34	16	Q8X4V1	Q8x4v1 escherichia
749	3	10.0	34	16	Q8U5V2	Q8u5v2 agrobacteri
750	3	10.0	34	16	Q8VIY1	Q8viy1 mycobacteri
751	3	10.0	34	16	Q8RIC7	Q8ric7 fusobacteri
752	3	10.0	34	16	Q8NWX3	Q8nwx3 staphylococ
753	3	10.0	34	16	Q8NV10	Q8nv10 staphylococ
754	3	10.0	34	16	Q8KEQ8	Q8keq8 chlorobium
755	3	10.0	34	16	Q8KEL5	Q8kel5 chlorobium
756	3	10.0	34	16	Q8KDE4	Q8kde4 chlorobium
757	3	10.0	34	16	Q8F830	Q8f830 leptospira
758	3	10.0	34	16	Q8F827	Q8f827 leptospira
759	3	10.0	34	16	Q8F5Y7	Q8f5y7 leptospira
760	3	10.0	34	16	Q8F0V9	Q8f0v9 leptospira
761	3	10.0	34	16	Q8EZR6	Q8ezr6 leptospira
762	3	10.0	34	16	Q8EZ37	Q8ez37 leptospira
763	3	10.0	34	16	Q8EYG6	Q8eyg6 leptospira
764	3	10.0	34	16	Q8EXH6	Q8exh6 leptospira
765	3	10.0	34	16	Q8EXA8	Q8exa8 leptospira
766	3	10.0	34	16	Q8EJ65	Q8ej65 shewanella
767	3	10.0	34	16	Q8EI45	Q8ei45 shewanella
768	3	10.0	34	16	Q8EHU5	Q8ehu5 shewanella
769	3	10.0	34	16	Q8E8Y3	Q8e8y3 shewanella
770	3	10.0	34	16	Q8E8W3	Q8e8w3 shewanella
771	3	10.0	34	16	Q8E173	Q8e173 streptococc
772	3	10.0	34	16	Q8CRY3	Q8cry3 staphylococ
773	3	10.0	34	17	Q8U1I1	Q8uli1 pyrococcus
774	3	10.0	35	2	Q9R624	Q9r624 bacillus su
775	3	10.0	35	2	Q9JPG9	Q9jpg9 neisseria m
776	3	10.0	35	2	Q9R625	Q9r625 bacillus su
777	3	10.0	35	2	Q9X3D6	Q9x3d6 prochloroco
778	3	10.0	35	2	Q9R5I3	Q9r5i3 thermoanaer
779	3	10.0	35	2	Q9FCX4	Q9fcx4 clostridium
780	3	10.0	35	2	Q9XBK0	Q9xbk0 bacillus ce
781	3	10.0	35	2	Q53564	Q53564 neisseria g
782	3	10.0	35	2	Q46537	Q46537 bacteroides
783	3	10.0	35	2	Q9ZG35	Q9zg35 chlamydia t
784	3	10.0	35	2	Q9RHG5	Q9rhg5 bacillus ce
785	3	10.0	35	2	Q9R4A1	Q9r4a1 klebsiella
786	3	10.0	35	2	O30661	O30661 vibrio chol
787	3	10.0	35	2	Q9ZG68	Q9zg68 chlamydia t
788	3	10.0	35	2	Q8RKG3	Q8rkg3 clostridium
789	3	10.0	35	2	Q8RIW2	Q8riw2 clostridium
790	3	10.0	35	2	Q9R626	Q9r626 bacillus su
791	3	10.0	35	2	P81927	P81927 lactobacill
792	3	10.0	35	3	Q96UT3	Q96ut3 saccharomyc
793	3	10.0	35	4	Q9BVR9	Q9bvr9 homo sapien
794	3	10.0	35	4	Q13380	Q13380 homo sapien
795	3	10.0	35	4	Q9BS62	Q9bs62 homo sapien
796	3	10.0	35	4	Q13165	Q13165 homo sapien
797	3	10.0	35	4	Q13828	Q13828 homo sapien
798	3	10.0	35	4	Q13264	Q13264 homo sapien

799	3	10.0	35	4	Q15421	Q15421 homo sapien
800	3	10.0	35	4	Q9Y634	Q9y634 homo sapien
801	3	10.0	35	4	Q9BU09	Q9bu09 homo sapien
802	3	10.0	35	4	Q8IU77	Q8iu77 homo sapien
803	3	10.0	35	5	Q27754	Q27754 pisaster oc
804	3	10.0	35	5	Q9U780	Q9u780 boophilus a
805	3	10.0	35	5	Q26372	Q26372 tribolium c
806	3	10.0	35	5	Q9U782	Q9u782 boophilus m
807	3	10.0	35	5	Q9TVJ7	Q9tvj7 boophilus m
808	3	10.0	35	5	Q9U783	Q9u783 boophilus m
809	3	10.0	35	5	Q9U784	Q9u784 boophilus m
810	3	10.0	35	5	Q9U781	Q9u781 boophilus m
811	3	10.0	35	5	Q8IF21	Q8if21 trypanosoma
812	3	10.0	35	6	Q95N74	Q95n74 equus cabal
813	3	10.0	35	6	Q9MZA7	Q9mza7 sus scrofa
814	3	10.0	35	8	Q951Q6	Q951q6 protoptilum
815	3	10.0	35	8	Q8W7S9	Q8w7s9 colpomenia
816	3	10.0	35	8	Q9GF85	Q9gf85 ginkgo bilo
817	3	10.0	35	8	Q8W7T0	Q8w7t0 petalonia b
818	3	10.0	35	8	Q8W7S8	Q8w7s8 petalonia f
819	3	10.0	35	8	Q8WE70	Q8we70 miliaria ca
820	3	10.0	35	8	Q8W7S7	Q8w7s7 scytosiphon
821	3	10.0	35	8	Q9GF98	Q9gf98 ceratophyll
822	3	10.0	35	8	Q95766	Q95766 cerataphis
823	3	10.0	35	8	Q94P82	Q94p82 corallium r
824	3	10.0	35	8	Q8WEJ7	Q8wej7 cycas circi
825	3	10.0	35	8	Q951S7	Q951s7 anthothela
826	3	10.0	35	8	Q951R1	Q951r1 narella nut
827	3	10.0	35	8	Q951S1	Q951s1 corallium k
828	3	10.0	35	8	Q8WII3	Q8wii3 colpomenia
829	3	10.0	35	8	Q951R3	Q951r3 anthomurice
830	3	10.0	35	8	Q8WIIH9	Q8wih9 scytosiphon
831	3	10.0	35	8	Q8WIIH5	Q8wih5 hydroclathr
832	3	10.0	35	8	Q951S9	Q951s9 protodendro
833	3	10.0	35	8	Q8WII1	Q8wii1 scytosiphon
834	3	10.0	35	8	Q951Q9	Q951q9 narella sp.
835	3	10.0	35	8	Q951S4	Q951s4 paragorgia
836	3	10.0	35	8	Q951R5	Q951r5 corallium s
837	3	10.0	35	10	Q9SPU2	Q9spu2 arabidopsis
838	3	10.0	35	10	Q9MAB1	Q9mab1 arabidopsis
839	3	10.0	35	10	Q9ZUW2	Q9zuw2 arabidopsis
840	3	10.0	35	10	P92971	P92971 arabidopsis
841	3	10.0	35	10	Q9LV08	Q9lv08 arabidopsis
842	3	10.0	35	10	Q9LQ64	Q9lq64 arabidopsis
843	3	10.0	35	10	Q94IS4	Q94is4 pinus radia
844	3	10.0	35	10	Q39297	Q39297 brassica na
845	3	10.0	35	10	Q8RVJ7	Q8rvj7 populus eur
846	3	10.0	35	10	Q9FJ84	Q9fj84 arabidopsis
847	3	10.0	35	10	Q8GUX4	Q8gux4 picea maria
848	3	10.0	35	11	Q63397	Q63397 rattus norv
849	3	10.0	35	11	Q9JLA4	Q9jla4 mus musculu
850	3	10.0	35	11	Q60608	Q60608 mus musculu
851	3	10.0	35	11	Q9QV50	Q9qv50 rattus sp.
852	3	10.0	35	11	Q922H5	Q922h5 mus musculu
853	3	10.0	35	11	Q8BK89	Q8bk89 mus musculu
854	3	10.0	35	12	Q90151	Q90151 bombyx mori
855	3	10.0	35	12	Q65380	Q65380 banana bunc

856	3	10.0	35	12	Q83333	Q83333 murine hepa
857	3	10.0	35	12	O55549	O55549 measles vir
858	3	10.0	35	12	Q8BB50	Q8bb50 human papil
859	3	10.0	35	13	Q90XB5	Q90xb5 xenopus lae
860	3	10.0	35	13	P83224	P83224 oxyuranus m
861	3	10.0	35	13	P83225	P83225 oxyuranus s
862	3	10.0	35	13	P83227	P83227 oxyuranus m
863	3	10.0	35	13	P83228	P83228 oxyuranus s
864	3	10.0	35	13	P83229	P83229 oxyuranus s
865	3	10.0	35	13	P83226	P83226 oxyuranus s
866	3	10.0	35	15	Q75981	Q75981 human immun
867	3	10.0	35	15	Q70328	Q70328 human immun
868	3	10.0	35	15	Q70380	Q70380 human immun
869	3	10.0	35	15	Q70319	Q70319 human immun
870	3	10.0	35	15	Q79465	Q79465 human immun
871	3	10.0	35	15	Q70426	Q70426 human immun
872	3	10.0	35	15	Q9J3S2	Q9j3s2 human immun
873	3	10.0	35	15	O71950	O71950 human immun
874	3	10.0	35	15	Q9IPY2	Q9ipy2 human immun
875	3	10.0	35	15	Q80574	Q80574 human immun
876	3	10.0	35	15	Q70425	Q70425 human immun
877	3	10.0	35	15	Q70362	Q70362 human immun
878	3	10.0	35	15	Q80601	Q80601 human immun
879	3	10.0	35	15	Q8QDX6	Q8qdx6 human immun
880	3	10.0	35	15	Q77702	Q77702 human immun
881	3	10.0	35	15	Q9QFA0	Q9qfa0 human immun
882	3	10.0	35	15	Q70330	Q70330 human immun
883	3	10.0	35	15	Q77584	Q77584 human immun
884	3	10.0	35	15	Q70317	Q70317 human immun
885	3	10.0	35	15	Q70316	Q70316 human immun
886	3	10.0	35	15	Q70402	Q70402 human immun
887	3	10.0	35	15	Q9YM80	Q9ym80 human immun
888	3	10.0	35	15	Q8QDY0	Q8qdy0 human immun
889	3	10.0	35	15	Q75970	Q75970 human immun
890	3	10.0	35	15	Q70409	Q70409 human immun
891	3	10.0	35	15	Q70325	Q70325 human immun
892	3	10.0	35	15	Q9YM17	Q9ym17 human immun
893	3	10.0	35	15	Q79468	Q79468 human immun
894	3	10.0	35	15	Q9YM96	Q9ym96 human immun
895	3	10.0	35	15	Q70363	Q70363 human immun
896	3	10.0	35	15	Q70321	Q70321 human immun
897	3	10.0	35	15	Q9YM22	Q9ym22 human immun
898	3	10.0	35	15	Q75990	Q75990 human immun
899	3	10.0	35	15	Q70323	Q70323 human immun
900	3	10.0	35	15	Q75989	Q75989 human immun
901	3	10.0	35	15	Q70428	Q70428 human immun
902	3	10.0	35	15	Q9YM67	Q9ym67 human immun
903	3	10.0	35	15	Q77585	Q77585 human immun
904	3	10.0	35	15	Q70403	Q70403 human immun
905	3	10.0	35	15	Q70327	Q70327 human immun
906	3	10.0	35	15	Q77250	Q77250 human immun
907	3	10.0	35	15	Q75955	Q75955 human immun
908	3	10.0	35	15	Q9IPY4	Q9ipy4 human immun
909	3	10.0	35	15	Q70424	Q70424 human immun
910	3	10.0	35	15	Q77582	Q77582 human immun
911	3	10.0	35	16	O07593	O07593 bacillus su
912	3	10.0	35	16	Q9KR18	Q9kr18 vibrio chol

913	3	10.0	35	16	Q9KNU1	Q9knul vibrio chol
914	3	10.0	35	16	Q9JWX5	Q9jwx5 neisseria m
915	3	10.0	35	16	Q9JV38	Q9jv38 neisseria m
916	3	10.0	35	16	Q9A427	Q9a427 caulobacter
917	3	10.0	35	16	Q9K241	Q9k241 chlamydia p
918	3	10.0	35	16	Q8XZB7	Q8xzb7 ralstonia s
919	3	10.0	35	16	Q8KCA6	Q8kca6 chlorobium
920	3	10.0	35	16	Q8G2D4	Q8g2d4 brucella su
921	3	10.0	35	16	Q8F9H5	Q8f9h5 leptospira
922	3	10.0	35	16	Q8F8D4	Q8f8d4 leptospira
923	3	10.0	35	16	Q8F1W8	Q8f1w8 leptospira
924	3	10.0	35	16	Q8EYH6	Q8eyh6 leptospira
925	3	10.0	35	16	Q8EGT2	Q8egt2 shewanella
926	3	10.0	35	16	Q8EGC0	Q8egc0 shewanella
927	3	10.0	35	16	Q8EG97	Q8eg97 shewanella
928	3	10.0	35	16	Q8EEP3	Q8eep3 shewanella
929	3	10.0	35	16	Q8E9Z1	Q8e9z1 shewanella
930	3	10.0	35	16	Q8DUY1	Q8duy1 streptococc
931	3	10.0	35	17	Q9HMP1	Q9hmp1 halobacteri
932	3	10.0	35	17	Q8ZXX9	Q8zxx9 pyrobaculum
933	3	10.0	36	2	O06954	O06954 salmonella
934	3	10.0	36	2	Q8VTS7	Q8vts7 listeria in
935	3	10.0	36	2	Q9ZG79	Q9zg79 chlamydia t
936	3	10.0	36	2	Q9RHE3	Q9rhe3 pediococcus
937	3	10.0	36	2	Q8VTS5	Q8vts5 listeria we
938	3	10.0	36	2	Q44437	Q44437 agrobacteri
939	3	10.0	36	2	Q9LB55	Q9lb55 helicobacte
940	3	10.0	36	2	Q48507	Q48507 lactococcus
941	3	10.0	36	2	Q99094	Q99094 salmonella
942	3	10.0	36	2	Q9S635	Q9s635 prochloroco
943	3	10.0	36	2	Q8VTR8	Q8vtr8 listeria iv
944	3	10.0	36	2	Q8VTS0	Q8vts0 listeria mo
945	3	10.0	36	2	Q8KYW1	Q8kyw1 uncultured
946	3	10.0	36	2	Q9R4X9	Q9r4x9 azotobacter
947	3	10.0	36	2	Q9R5L0	Q9r5l0 sarcina ven
948	3	10.0	36	2	Q9X3G2	Q9x3g2 prochloroco
949	3	10.0	36	2	Q9R536	Q9r536 sphingomona
950	3	10.0	36	2	Q8GRH1	Q8grh1 peptobacter
951	3	10.0	36	3	Q96W36	Q96w36 ophiostoma
952	3	10.0	36	4	Q9UNV7	Q9unv7 homo sapien
953	3	10.0	36	4	Q9P1E9	Q9ple9 homo sapien
954	3	10.0	36	4	Q9UPB7	Q9upb7 homo sapien
955	3	10.0	36	4	Q8NE47	Q8ne47 homo sapien
956	3	10.0	36	5	Q9GSY9	Q9gsy9 carcinus ma
957	3	10.0	36	5	Q9NGN1	Q9ngn1 strongyloce
958	3	10.0	36	5	Q27730	Q27730 plasmodium
959	3	10.0	36	5	Q9GNP3	Q9gnp3 caenorhabdi
960	3	10.0	36	5	O01333	O01333 caenorhabdi
961	3	10.0	36	5	Q25781	Q25781 plasmodium
962	3	10.0	36	5	Q8ISR7	Q8isr7 spodoptera
963	3	10.0	36	5	Q8IGF5	Q8igf5 drosophila
964	3	10.0	36	6	O97889	O97889 pongo pygma
965	3	10.0	36	6	Q29059	Q29059 sus scrofa
966	3	10.0	36	6	Q9XT44	Q9xt44 pongo pygma
967	3	10.0	36	6	Q9N1C5	Q9n1c5 bos taurus
968	3	10.0	36	6	O97890	O97890 pan troglod
969	3	10.0	36	6	P79428	P79428 capra hircu

970	3	10.0	36	8	063675	063675 emberiza pu
971	3	10.0	36	8	Q9GF81	Q9gf81 gnetum gnem
972	3	10.0	36	8	Q9TIE4	Q9tie4 hydrocotyle
973	3	10.0	36	8	Q9TIF1	Q9tif1 bolax gummi
974	3	10.0	36	8	Q9GFA3	Q9gfa3 cabomba car
975	3	10.0	36	8	Q9GF97	Q9gf97 ceratophyll
976	3	10.0	36	8	Q94VL4	Q94vl4 salmo trutt
977	3	10.0	36	8	Q36303	Q36303 musa schizo
978	3	10.0	36	8	Q9TIF0	Q9tif0 klotzschia
979	3	10.0	36	8	Q94NY5	Q94ny5 salmo salar
980	3	10.0	36	8	Q9GF76	Q9gf76 lactoris fe
981	3	10.0	36	8	Q9MSP9	Q9msp9 nymphaea od
982	3	10.0	36	8	Q9TIF3	Q9tif3 eremocharis
983	3	10.0	36	8	Q9GF74	Q9gf74 liriodendro
984	3	10.0	36	8	Q9TIE2	Q9tie2 aralia chin
985	3	10.0	36	8	Q9TIF2	Q9tif2 azurella tr
986	3	10.0	36	8	Q9GF89	Q9gf89 drimys wint
987	3	10.0	36	8	Q9MSR0	Q9msr0 zamia furfu
988	3	10.0	36	8	063650	063650 emberiza sc
989	3	10.0	36	8	Q9TIE3	Q9tie3 hydrocotyle
990	3	10.0	36	8	Q9TIE5	Q9tie5 xanthosia a
991	3	10.0	36	8	Q9GFA9	Q9gfa9 acorus cala
992	3	10.0	36	8	Q8HS50	Q8hs50 ascarina lu
993	3	10.0	36	8	Q8HS46	Q8hs46 austrobaile
994	3	10.0	36	8	Q8HS42	Q8hs42 chloranthus
995	3	10.0	36	8	Q8HS31	Q8hs31 lilium supe
996	3	10.0	36	8	Q8HS27	Q8hs27 magnolia st
997	3	10.0	36	8	Q8HS18	Q8hs18 sagittaria
998	3	10.0	36	8	Q8HKF5	Q8hkf5 rhipicephal
999	3	10.0	36	8	Q8HKC6	Q8hkc6 haemaphysal
1000	3	10.0	36	10	Q38977	Q38977 arabidopsis

ALIGNMENTS

RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.

AC Q91Y90;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Parathyroid hormone (Fragment).

GN PTH.

OS Peromyscus maniculatus (Deer mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Peromyscus.

OX NCBI_TaxID=10042;

RN [1]

RP SEQUENCE FROM N.A.

RA Prince K.L., Dewey M.J.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF382953; AAK63072.1; -.

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; Pthyrrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 46.7%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||||||
Db 14 VSEIQLMHNLGKHL 27

RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382952; AAK63071.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 46.7%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||||||
Db 14 VSEIQLMHNLGKHL 27

RESULT 3

O17148

ID O17148 PRELIMINARY; PRT; 34 AA.
AC O17148;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359533; PubMed=8078520;
 RA Frosch P., Hartmann M., Muhlschlegel F., Frosch M.;
 RT "Sequence heterogeneity of the echinococcal antigen B."
 RL Mol. Biochem. Parasitol. 64:171-175(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence."
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;

Query Match 16.7%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
 |||||
 Db 15 LRKKL 19

RESULT 4

Q97K50

ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007622; AAK79045.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 16.7%; Score 5; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 5

Q9HR65

ID Q9HR65 PRELIMINARY; PRT; 34 AA.
AC Q9HR65;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrojna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 16.7%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
|||||
Db 26 LRKKL 30

RESULT 6

Q8BTB9

ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK011220; BAC25325.1; -.
 SQ SEQUENCE 35 AA; 3967 MW; F81156686390ECD8 CRC64;

Query Match 16.7%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5
 ||||
 Db 2 SVSEI 6

RESULT 7

Q97RG6

ID Q97RG6 PRELIMINARY; PRT; 35 AA.
 AC Q97RG6;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0853.
 GN SP0853.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).

DR EMBL; AE007391; AAK74982.1; -.
DR TIGR; SP0853; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;

Query Match 16.7%; Score 5; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 8

O24285

ID O24285 PRELIMINARY; PRT; 28 AA.
AC O24285;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LFY protein (Fragment).
GN LFY.
OS Pinus radiata (Monterey pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vegetative;
RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
RT "Partial characterization of Pinus radiata meristem identity homolog
RT gene (LFY).";
RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U66725; AAB06792.1; -.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 13.3%; Score 4; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 9

Q8GZQ8

ID Q8GZQ8 PRELIMINARY; PRT; 28 AA.
AC Q8GZQ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SNF-1 related kinase (Fragment).
GN BKIN12.

OS *Hordeum vulgare* var. *distichum* (Two-rowed barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=112509;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Igri;
 RA Clark J.S.C., Dani M., Barker J.H.A., Halford N.G., Karp A.;
 RT "Bkin12 Promoter Variants - Examples of Functional Biodiversity?";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF448389; AAN76447.1; -.
 KW Kinase.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2950 MW; 853EDC11F6BB2C6C CRC64;

Query Match 13.3%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 18 NLGK 21

RESULT 10

Q49148

ID Q49148 PRELIMINARY; PRT; 29 AA.
 AC Q49148;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE PQQ biosynthesis polypeptide.
 GN PQQD.
 OS *Methylobacterium extorquens*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Methylobacteriaceae; *Methylobacterium*.
 OX NCBI_TaxID=408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AM1;
 RX MEDLINE=94179111; PubMed=8132470;
 RA Morris C.J., Biville F., Turlin E., Lee E., Ellermann K., Fan W.H.,
 RA Ramamoorthi R., Springer A.L., Lidstrom M.E.;
 RT "Isolation, phenotypic characterization, and complementation analysis
 RT of mutants of *Methylobacterium extorquens* AM1 unable to synthesize
 RT pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.";
 RL J. Bacteriol. 176:1746-1755(1994).
 DR EMBL; L25889; AAA17878.1; -.
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;

Query Match 13.3%; Score 4; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||

Db

8 VSEI 11

RESULT 11

Q9UCL2

ID Q9UCL2 PRELIMINARY; PRT; 29 AA.
AC Q9UCL2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Renal intestinal-type alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney.";
RL Clin. Chem. 38:2539-2542(1992).
DR InterPro; IPR001952; Alk_phosphatase.
DR ProDom; PD001868; Alk_phosphatase; 1.
SQ SEQUENCE 29 AA; 3250 MW; 30501BB7BEEAD8D0 CRC64;

Query Match 13.3%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29

||||

Db 23 KKLQ 26

RESULT 12

Q96PP3

ID Q96PP3 PRELIMINARY; PRT; 29 AA.
AC Q96PP3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lympho-epithelial Kazal type-related inhibitor LEKTI (Fragment).
GN SPINK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sprecher E., Chavanas S., DiGiovanna J.J., Amin S., Nielsen K.,
RA Prendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig E.,
RA de Luna M.L., Williams M.L., Buehler B., Pfendner E., Bale S.J.,
RA Uitto J., Hovnanian A., Richard G.;
RT "The spectrum of pathogenic mutations in SPINK 5 in 19 families with
RT Netherton syndrome - Implications for mutation detection and first

RT case of prenatal diagnosis.";
RL J. Invest. Dermatol. 0:0-0(2001).
DR EMBL; AF295783; AAK97140.1; -.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3449 MW; 9F31E2AD857EC1BB CRC64;

Query Match 13.3%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
|||
Db 14 NLGK 17

RESULT 13

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.
AC Q25603;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tubulin.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RA Chandrashekar R., Curtis K.C., Weil G.J.;
RT "Onchocerca volvulus cDNA clone."
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U15095; AAA50364.1; -.
SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 13.3%; Score 4; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 4 VSEI 7

RESULT 14

O13043

ID O13043 PRELIMINARY; PRT; 29 AA.
AC O13043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;

OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268658; PubMed=9108066;
 RA Schlake T., Schorpp M., Nehls M., Boehm T.;
 RT "The nude gene encodes a sequence-specific DNA binding protein with
 RT homologs in organisms that lack an anticipatory immune system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
 DR EMBL; Y11539; CAA72302.1; -.
 DR InterPro; IPR001766; TF_Fork_head.
 DR Pfam; PF00250; Fork_head; 1.
 DR ProDom; PD000425; TF_Fork_head; 1.
 FT NON_TER 1 1
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 13.3%; Score 4; DB 13; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
 ||||
 Db 17 VSEI 20

RESULT 15

Q9JMV3

ID Q9JMV3 PRELIMINARY; PRT; 30 AA.
 AC Q9JMV3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Luciferase alpha-subunit (Fragment).
 GN LUXA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RA Lotz W., Bauer T.;
 RT "luxAB/kan-cassette for site-directed insertion mutagenesis and
 RT bacterial transcription studies.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RA Olsson O., Koncz C., Szalay A.;
 RT "The use of luxA gene of the bacterial luciferase operon as a reporter
 RT gene.";
 RL Mol. Gen. Genet. 215:1-9(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RX MEDLINE=92114868; PubMed=1685011;

RA Escher A., O'Kane D.J., Szalay A.;
 RT "The beta subunit polypeptide of *Vibrio harveyi* luciferase determines
 RT light emission at 42 degrees C.";
 RL Mol. Gen. Genet. 230:385-393(1991).
 DR EMBL; AJ249443; CAB96206.1; -.
 DR HSSP; P07740; 1LUC.
 DR InterPro; IPR002103; Bac_luciferase.
 DR Pfam; PF00296; bac_luciferase; 1.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3454 MW; 2FC87235BDBE72FD CRC64;

Query Match 13.3%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 26 NLGK 29

RESULT 16

Q9UBV5

ID Q9UBV5 PRELIMINARY; PRT; 30 AA.
 AC Q9UBV5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Intestinal alkaline phosphatase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney.";
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatase.
 DR ProDom; PD001868; Alk_phosphatase; 1.
 SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BEB9BDE6 CRC64;

Query Match 13.3%; Score 4; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 24 KKLQ 27

RESULT 17

Q8DZP7

ID Q8DZP7 PRELIMINARY; PRT; 30 AA.
 AC Q8DZP7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN SAG1053.
 OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=22222988; PubMed=12200547;
 RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AE014240; AAM99934.1; -.
 DR TIGR; SAG1053; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 13.3%; Score 4; DB 16; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 23 KKLQ 26

RESULT 18

Q55314

ID Q55314 PRELIMINARY; PRT; 31 AA.
 AC Q55314;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Urf2 protein (Fragment).
 GN URF2.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96085144; PubMed=8521845;
 RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;
 RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate

RT dehydrogenase genes from the thermophilic archaeon Sulfolobus
 RT solfataricus overlap by 8bp. Isolation, sequencing of the genes and
 RT expression on Escherichia coli.";
 RL Eur. J. Biochem. 233:800-808(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94082761; PubMed=8259927;
 RA Arcari P., Russo A.D., Ianniciello G., Gallo M., Bocchini V.;
 RT "Nucleotide sequence and molecular evolution of the gene coding for
 RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic
 RT archaeobacterium Sulfolobus solfataricus.";
 RL Biochem. Genet. 31:241-251(1993).
 DR EMBL; X80178; CAA56461.1; -.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 13.3%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
 Db 11 WLRK 14

RESULT 19

Q8NEI8

ID Q8NEI8 PRELIMINARY; PRT; 31 AA.
 AC Q8NEI8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030993; AAH30993.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;

Query Match 13.3%; Score 4; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 18 VSEI 21

RESULT 20

Q9MS77

ID Q9MS77 PRELIMINARY; PRT; 31 AA.
AC Q9MS77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Photosystem I protein M.
GN PSAM.
OS Phacus acuminata.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Phacus.
OX NCBI_TaxID=130316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21080550; PubMed=11212923;
RA Doetsch N.A., Thompson M.D., Favreau M.R., Hallick R.B.;
RT "Comparison of psbK operon organization and group III intron content
RT in chloroplast genomes of 12 Euglenoid species.";
RL Mol. Gen. Genet. 264:682-690(2001).
DR EMBL; AF241276; AAF82438.1; -.
KW Chloroplast.
SQ SEQUENCE 31 AA; 3449 MW; 2FFB2AF4B4ACDEC8 CRC64;

Query Match 13.3%; Score 4; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
|||
Db 24 NLGK 27

RESULT 21

O50669

ID O50669 PRELIMINARY; PRT; 31 AA.
AC O50669;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BBH11.
GN BBH11.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid lp28-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;

RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
DR EMBL; AE000784; AAC66002.1; -.
DR TIGR; BBH11; -.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;

Query Match 13.3%; Score 4; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 26 KKLQ 29

RESULT 22

Q9QZQ2

ID Q9QZQ2 PRELIMINARY; PRT; 32 AA.
AC Q9QZQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neurotensin receptor (Fragment).
GN NTSR OR NTR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=99445567; PubMed=10514493;
RA Tavares D., Tully K., Dobner P.R.;
RT "Sequences required for induction of neurotensin receptor gene
RT expression during neuronal differentiation of N1E-115 neuroblastoma
RT cells.";
RL J. Biol. Chem. 274:30066-30079(1999).
DR EMBL; AF172326; AAD51806.1; -.
DR MGD; MGI:97386; Ntsr.
KW Receptor.
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;

Query Match 13.3%; Score 4; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17
|||
Db 2 HLNS 5

RESULT 23

Q9HSZ0

ID Q9HSZ0 PRELIMINARY; PRT; 32 AA.

AC Q9HSZ0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Vng0019h.
 GN VNG0019H.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE004971; AAG18659.1; -.
 KW Complete proteome.
 SQ SEQUENCE 32 AA; 3758 MW; 22D669246C97A817 CRC64;

 Query Match 13.3%; Score 4; DB 17; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
 ||||
 Db 13 KLQD 16

RESULT 24

Q95SD4

ID Q95SD4 PRELIMINARY; PRT; 33 AA.
 AC Q95SD4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE GM02640p.
 GN BCDNA:GM02640.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY060847; AAL28395.1; -.
DR FlyBase; FBgn0047288; BcDNA:GM02640.
SQ SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBE4A7 CRC64;

Query Match 13.3%; Score 4; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 21 KKLQ 24

RESULT 25

Q9PKX3

ID Q9PKX3 PRELIMINARY; PRT; 33 AA.
AC Q9PKX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein TC0337.
GN TC0337.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002301; AAF39200.1; -.
DR TIGR; TC0337; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 13.3%; Score 4; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 26 LRKK 29

RESULT 26

Q9ZG81

ID Q9ZG81 PRELIMINARY; PRT; 34 AA.
AC Q9ZG81;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE ATP-dependent permease (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF087260; AAD04038.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 13.3%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKK 27
 ||||
 Db 25 LRKK 28

RESULT 27

Q8GFK2

ID Q8GFK2 PRELIMINARY; PRT; 34 AA.
 AC Q8GFK2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ORF37.
 OS Staphylococcus aureus.
 OG Plasmid EDINA plasmid.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-1;
 RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
 RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
 RT plasmid."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP003089; BAC54529.1; -.
 KW Plasmid.
 SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 13.3%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
 ||||
 Db 6 KKLQ 9

RESULT 28

Q8C4P4

ID Q8C4P4 PRELIMINARY; PRT; 34 AA.
 AC Q8C4P4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Zinc finger homeodomain 4 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK081561; BAC38260.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3755 MW; EF41DCAF348467B0 CRC64;

Query Match 13.3%; Score 4; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
 ||||
 Db 2 KLQD 5

RESULT 29

Q90ZJ4

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
 AC Q90ZJ4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain long form (Fragment).
 GN PDGF-A.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363439; PubMed=11470524;
 RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
 RT "Characterization and expression of three forms of cDNA encoding
 RT chicken platelet-derived growth factor-A chain.";
 RL Gene 272:181-190(2001).

DR EMBL; AB031024; BAB62544.1; -.
FT NON_TER 1 1
SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 13.3%; Score 4; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKKL 28
|||
Db 28 RKKL 31

RESULT 30

Q98FK5

ID Q98FK5 PRELIMINARY; PRT; 34 AA.
AC Q98FK5;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein msr3733.
GN MSR3733.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003002; BAB50562.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 34 AA; 3804 MW; D6AAA82ECB590413 CRC64;

Query Match 13.3%; Score 4; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
|||
Db 28 KLQD 31

RESULT 31

Q8G2Q2

ID Q8G2Q2 PRELIMINARY; PRT; 34 AA.
AC Q8G2Q2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN BR0266.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014339; AAN29215.1; -.
 DR TIGR; BR0266; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 34 AA; 3781 MW; 76E820326E6CA66E CRC64;

Query Match 13.3%; Score 4; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGKH 14
 ||||
 Db 10 LGKH 13

RESULT 32

Q8V6J8

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.
 AC Q8V6J8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 4.1 kDa protein.
 OS Halovirus HF2.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 OX NCBI_TaxID=33771;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyal-Smith M.L.;
 RT "Sequence and transcription of halovirus HF2."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF222060; AAL55025.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 35 AA; 4115 MW; 2652C319622E9CE4 CRC64;

Query Match 13.3%; Score 4; DB 12; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 10 SVSE 13

RESULT 33

Q9KQG4

ID Q9KQG4 PRELIMINARY; PRT; 35 AA.
AC Q9KQG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein VC2034.
GN VC2034.
OS *Vibrio cholerae*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
RT *cholerae*."
RL Nature 406:477-483(2000).
DR EMBL; AE004278; AAF95182.1; -.
DR TIGR; VC2034; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 35 AA; 4181 MW; D185B6339A711D54 CRC64;

Query Match 13.3%; Score 4; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 24 KKLQ 27

RESULT 34

Q8F102

ID Q8F102 PRELIMINARY; PRT; 35 AA.
AC Q8F102;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA3339.
OS *Leptospira interrogans*.

OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE011494; AAN50536.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB32E980B CRC64;

Query Match 13.3%; Score 4; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 HLNS 17
 ||||
 Db 3 HLNS 6

RESULT 35

Q53920

ID Q53920 PRELIMINARY; PRT; 36 AA.
 AC Q53920;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE OrfA protein (Fragment).
 GN ORFA.
 OS Streptomyces chrysomallus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1899;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341259; PubMed=8062824;
 RA Pahl A., Keller U.;
 RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
 RT of two FK506-binding domains with its gene transcriptionally coupled
 RT to the FKBP-12 gene."
 RL EMBO J. 13:3472-3480(1994).
 DR EMBL; Z34523; CAA84281.1; -.
 DR InterPro; IPR004347; DUF245.
 DR Pfam; PF03136; DUF245; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 36 AA; 4121 MW; EBD470AAF99A728E CRC64;

Query Match 13.3%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ERVE 22
 ||||
 Db 27 ERVE 30

RESULT 36

O68941

ID O68941 PRELIMINARY; PRT; 36 AA.
AC O68941;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dinitrogenase 3 beta subunit (Fragment).
GN ANFK.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE FROM N.A.
RA Loveless T.M., Bishop P.E.;
RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems
RT in Diverse Diazotrophs.";
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF058778; AAC14327.1; -.
DR InterPro; IPR000510; Oxred_nitrognse1.
DR Pfam; PF00148; oxidored_nitro; 1.
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFD437D97 CRC64;

Query Match 13.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 5 LRKK 8

RESULT 37

Q8WXW8

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.
AC Q8WXW8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Urea transporter JK glycoprotein (Fragment).
GN JK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;
RT "Molecular Basis of the Jk(a-b-) Phenotype in Non-Finnish European
RT Pedigrees.";
RL Br. J. Haematol. 0:0-0(2001).
DR EMBL; AF328890; AAL37474.1; -.
DR InterPro; IPR004937; Urea_transporter.
DR Pfam; PF03253; UT; 1.
FT NON_TER 1 1
SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;

Query Match 13.3%; Score 4; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNSM 18
|||
Db 7 LNSM 10

RESULT 38

Q9SJ63

ID Q9SJ63 PRELIMINARY; PRT; 36 AA.
AC Q9SJ63;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE At2g35870 protein.
GN AT2G35870.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC007017; AAD21470.1; -.
SQ SEQUENCE 36 AA; 4358 MW; DC966779BBD6B834 CRC64;

Query Match 13.3%; Score 4; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 4 KKLQ 7

RESULT 39

Q9PXD1

ID Q9PXD1 PRELIMINARY; PRT; 36 AA.
AC Q9PXD1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Genome polyprotein [Contains: envelope glycoprotein E2/NS1 (GP68)]
DE (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96343121; PubMed=8750162;
RA Chayama K., Tsubota A., Arase Y., Saitoh S., Ikeda K., Matsumoto T.,
RA Hashimoto M., Kobayashi M., Kanda M., Morinaga T.;
RT "Genotype, slow decrease in virus titer during interferon treatment
RT and high degree of sequence variability of hypervariable region are
RT indicative of poor response to interferon treatment in patients with
RT chronic hepatitis type C.";
RL J. Hepatol. 23:648-653(1995).
DR InterPro; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 36 AA; 3546 MW; 5BB7935A55048D34 CRC64;

Query Match 13.3%; Score 4; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLM 8
|||
Db 33 IQLM 36

RESULT 40

Q91D77
ID Q91D77 PRELIMINARY; PRT; 36 AA.
AC Q91D77;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ORF2 hypothetical protein, isolate:HM0319 (Fragment).
OS TTV-like mini virus.
OC Viruses; ssDNA viruses; Circoviridae.
OX NCBI_TaxID=93678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM0319;
RA Michitaka K., Matsubara H., Horiike N., Kihana T., Yano M., Mori T.,
RA Onji M.;
RT "Existence of TT virus DNA and TTV-like mini virus DNA in infant cord
RT blood.";
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB059561; BAB69654.1; -.
DR InterPro; IPR004118; TT_ORF2.

DR Pfam; PF02957; TT_ORF2; 1.

KW Hypothetical protein.

FT NON_TER 36 36

SQ SEQUENCE 36 AA; 4291 MW; 92145F475EA841F1 CRC64;

Query Match 13.3%; Score 4; DB 12; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29

||||

Db 14 KKLQ 17

Search completed: January 14, 2004, 10:41:57

Job time : 23.4299 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 4.95327 Seconds
(without alignments)
284.822 Million cell updates/sec

Title: US-09-843-221A-166
Perfect score: 30
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	5	16.7	33	1	FABI_RHASA	P81175 rhamdia sap
2	4	13.3	29	1	DMD_RAT	P11530 rattus norv
3	4	13.3	39	1	SR1C_SARPE	P08377 sarcophaga
4	3	10.0	28	1	CH60_MYCSM	P80673 mycobacteri
5	3	10.0	28	1	COXB_SOLTU	P80499 solanum tub
6	3	10.0	28	1	GUN_SCHCO	P81190 schizophyll
7	3	10.0	28	1	PA23_TRIST	P82894 trimeresuru
8	3	10.0	28	1	PA2C_PSEPO	P20260 pseudechis
9	3	10.0	28	1	VI03_VACCP	Q00334 vaccinia vi
10	3	10.0	28	1	VIP_ALLMI	P48142 alligator m
11	3	10.0	28	1	VIP_RANRI	P81016 rana ridibu
12	3	10.0	28	1	VIP_SHEEP	P04565 ovis aries
13	3	10.0	29	1	GALA_ALLMI	P47215 alligator m
14	3	10.0	29	1	GALA_AMICA	P47214 amia calva
15	3	10.0	29	1	GALA_CHICK	P30802 gallus gall
16	3	10.0	29	1	GALA_ONCMY	P47213 oncorhynch
17	3	10.0	29	1	GALA_RANRI	P47216 rana ridibu

18	3	10.0	29	1	GALA_SHEEP	P31234	ovis aries
19	3	10.0	29	1	GLUC_CHIBR	P31297	chinchilla
20	3	10.0	29	1	IPYR_DESVH	P19371	desulfovibr
21	3	10.0	29	1	NUO1_SOLTU	P80267	solanum tub
22	3	10.0	29	1	P2SM_LOXIN	P83046	loxosceles
23	3	10.0	29	1	PCG4_PACGO	P82417	pachycondyl
24	3	10.0	29	1	RS7_METTE	O93639	methanosarc
25	3	10.0	29	1	SODC_OLEEU	P80740	olea europa
26	3	10.0	29	1	TL16_SPIOL	P81834	spinacia ol
27	3	10.0	30	1	DMS3_PHYSA	P80279	phyllomedus
28	3	10.0	30	1	FTN_BACFR	P28733	bacteroides
29	3	10.0	30	1	GLUM_ANGAN	P41521	anguilla an
30	3	10.0	30	1	OTCC_AERPU	P11726	aeromonas p
31	3	10.0	30	1	PCG2_PACGO	P82415	pachycondyl
32	3	10.0	30	1	PCG3_PACGO	P82416	pachycondyl
33	3	10.0	30	1	PSAM_PORPU	P51395	porphyra pu
34	3	10.0	30	1	TX2_THRPR	P83476	thrixopelma
35	3	10.0	30	1	UP61_UPEIN	P82037	uperoleia i
36	3	10.0	30	1	UP62_UPEIN	P82038	uperoleia i
37	3	10.0	30	1	VAA2_EQUAR	Q04238	equisetum a
38	3	10.0	30	1	Y523_BORBU	O51473	borrelia bu
39	3	10.0	31	1	CEC1_PIG	P14661	sus scrofa
40	3	10.0	31	1	CXMA_CONMR	P56708	conus marmo
41	3	10.0	31	1	DEJP_DROME	P81160	drosophila
42	3	10.0	31	1	DIUX_DIPPU	P82372	diploptera
43	3	10.0	31	1	H13_WHEAT	P15872	triticum ae
44	3	10.0	31	1	LPL_BUCRP	Q53017	buchnera ap
45	3	10.0	31	1	MALK_PHOLU	P41124	photorhabdu
46	3	10.0	31	1	NAP4_HUMAN	P19877	homo sapien
47	3	10.0	31	1	PETL_LOTJA	Q9bbr4	lotus japon
48	3	10.0	31	1	PETL_MARPO	P12179	marchantia
49	3	10.0	31	1	PETL_MESVI	Q9mun4	mesostigma
50	3	10.0	31	1	PETL_NEPOL	Q9tky9	nephroselmi
51	3	10.0	31	1	PSAM_EUGGR	P31479	euglena gra
52	3	10.0	31	1	SARL_MOUSE	Q9cqd6	mus musculu
53	3	10.0	31	1	SARL_RABIT	P42532	oryctolagus
54	3	10.0	31	1	SCK5_ANDMA	P31719	androctonus
55	3	10.0	31	1	SCKL_LEIQH	P16341	leiurus qui
56	3	10.0	31	1	Y822_BORBU	O51762	borrelia bu
57	3	10.0	32	1	ADHR_DROYA	P28487	drosophila
58	3	10.0	32	1	CAL2_ONCKE	P01264	oncorhynchu
59	3	10.0	32	1	CAL3_ONCKI	P01265	oncorhynchu
60	3	10.0	32	1	CAL_ANGJA	P01262	anguilla ja
61	3	10.0	32	1	COA2_BPIF1	O80296	bacterioph
62	3	10.0	32	1	CY31_DESAC	P81078	desulfuromo
63	3	10.0	32	1	FF21_SALEN	P55224	salmonella
64	3	10.0	32	1	IAPP_PIG	Q29119	sus scrofa
65	3	10.0	32	1	ITR3_CUCPE	P10293	cucurbita p
66	3	10.0	32	1	ITR4_CUCMA	P07853	cucurbita m
67	3	10.0	32	1	LEC_DOLAX	P02875	dolichos ax
68	3	10.0	32	1	MIFH_TRITR	P81748	trichuris t
69	3	10.0	32	1	P1SM_LOXIN	P83045	loxosceles
70	3	10.0	32	1	PETM_GUIITH	O78499	guillardia
71	3	10.0	32	1	PHSS_DESBN	P13064	desulfovibr
72	3	10.0	32	1	PSAM_MARPO	P31590	marchantia
73	3	10.0	32	1	PSBQ_PEA	P19589	pisum sativ
74	3	10.0	32	1	PSBT_ODOSI	P49516	odontella s

75	3	10.0	32	1	PSBZ_EUGST	Q8sl89	euglena ste
76	3	10.0	32	1	PSBZ_EUGVI	Q8sl87	euglena vir
77	3	10.0	32	1	Y160_BPT4	P39247	bacterioph
78	3	10.0	32	1	YCPG_MASLA	P29735	mastigoclad
79	3	10.0	33	1	GGN1_RANRU	P80395	rana rugosa
80	3	10.0	33	1	GLU2_ORENI	P81027	oreochromis
81	3	10.0	33	1	RUGB_RANRU	P80955	rana rugosa
82	3	10.0	33	1	T1F_PARTE	Q27172	paramecium
83	3	10.0	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
84	3	10.0	33	1	YC12_EUGGR	P31559	euglena gra
85	3	10.0	34	1	DMS1_PHYSA	P24302	phyllomedus
86	3	10.0	34	1	DMS2_PHYSA	P80278	phyllomedus
87	3	10.0	34	1	GAST_CAPHI	P04564	capra hircu
88	3	10.0	34	1	GUN1_SCLSC	P21833	sclerotinia
89	3	10.0	34	1	TX1_SCOGR	P56855	scodra gris
90	3	10.0	35	1	CECA_AEDAL	P81417	aedes albop
91	3	10.0	35	1	COPA_CANFA	P40765	canis famil
92	3	10.0	35	1	CPI2_PIG	P80736	sus scrofa
93	3	10.0	35	1	GP58_BPSP1	O48412	bacterioph
94	3	10.0	35	1	LEC1_CYTSE	P22970	cytisis ses
95	3	10.0	35	1	LEC3_ULLEU	P23032	ulex europe
96	3	10.0	35	1	NP30_STAAU	P21222	staphylococ
97	3	10.0	35	1	PBP_ORGPS	P34178	orgyia pseu
98	3	10.0	35	1	PETG_CYACA	Q9tlq9	cyanidium c
99	3	10.0	35	1	PSBM_SYNY3	P72701	synechocyst
100	3	10.0	35	1	RL15_SYNP7	P31160	synechococc
101	3	10.0	35	1	SCKK_TITSE	P56219	tityus serr
102	3	10.0	35	1	TX1_GRASP	P56852	grammostola
103	3	10.0	35	1	TX1_THRPR	P83480	thrixopelma
104	3	10.0	35	1	TX2_GRASP	P56853	grammostola
105	3	10.0	35	1	VORB_METTM	P80908	methanobact
106	3	10.0	35	1	YRKM_BACSU	P54440	bacillus su
107	3	10.0	36	1	ELH_THETS	P80594	theromyzon
108	3	10.0	36	1	NPF_ARTTR	P41334	artioposthi
109	3	10.0	36	1	OSTS_YEAST	Q99380	saccharomyc
110	3	10.0	36	1	PETM_SYNY3	P74810	synechocyst
111	3	10.0	36	1	R18A_BOVIN	P82919	bos taurus
112	3	10.0	36	1	RET4_CHICK	P30370	gallus gall
113	3	10.0	36	1	RL6_HALCU	P05968	halobacteri
114	3	10.0	36	1	Y260_BACHD	Q9kg53	bacillus ha
115	3	10.0	36	1	Y609_ARCFU	O29646	archaeoglob
116	3	10.0	37	1	DIU1_TENMO	P56618	tenebrio mo
117	3	10.0	37	1	IAPP_CRIGR	P19890	cricetulus
118	3	10.0	37	1	LCNM_LACLA	P83002	lactococcus
119	3	10.0	37	1	OGT1_RABIT	P81436	oryctolagus
120	3	10.0	37	1	PIP7_BOVIN	P21671	bos taurus
121	3	10.0	37	1	RL36_PASMU	P57942	pasteurella
122	3	10.0	37	1	SCKI_MESTA	P24663	mesobuthus
123	3	10.0	37	1	Y63_BPT3	P20328	bacterioph
124	3	10.0	38	1	CPRP_CANPG	P81033	cancer pagu
125	3	10.0	38	1	DNP_DENAN	P28374	dendroaspis
126	3	10.0	38	1	NLT1_VITSX	P80275	vitis sp. (
127	3	10.0	38	1	NLT2_VITSX	P33556	vitis sp. (
128	3	10.0	38	1	OBP2_HYSCR	P81648	hystrix cri
129	3	10.0	38	1	PYSA_METBA	P80521	methanosarc
130	3	10.0	38	1	RL36_ECOLI	P21194	escherichia
131	3	10.0	38	1	RL36_PSEAE	Q9hwf6	pseudomonas

132	3	10.0	38	1	RL36_THEMEA	Q9xli6	thermotoga
133	3	10.0	38	1	RL36_YERPE	Q8zj91	yersinia pe
134	3	10.0	38	1	RR12_PINCO	P49168	pinus conto
135	3	10.0	38	1	YJ39_ARCFU	O28340	archaeoglob
136	3	10.0	39	1	CEC_GLOMR	P83403	glossina mo
137	3	10.0	39	1	COLI_BALPH	P01195	balaenopter
138	3	10.0	39	1	COLI_RABIT	P06297	oryctolagus
139	3	10.0	39	1	COLI_SQUAC	P01197	squalus aca
140	3	10.0	39	1	COLI_STRCA	P01196	struthio ca
141	3	10.0	39	1	EXE3_HELHO	P20394	heloderma h
142	3	10.0	39	1	FUC3_RAT	P80349	rattus norv
143	3	10.0	39	1	GVPC_SPICC	P81000	spirulina s
144	3	10.0	39	1	H2A_BUFBG	P55897	bufo bufo g
145	3	10.0	39	1	LCGA_LACLA	P36961	lactococcus
146	3	10.0	39	1	PA2_AGKBI	Q9psf9	agkistrodon
147	3	10.0	39	1	PSBX_PORPU	P51197	porphyra pu
148	3	10.0	39	1	PSBY_SYNY3	P73676	synechocyst
149	3	10.0	40	1	ALB1_TRASC	P81188	trachemys s
150	3	10.0	40	1	HPT_RABIT	P19007	oryctolagus
151	3	10.0	40	1	HS9A_RABIT	P30946	oryctolagus
152	3	10.0	40	1	KAD_STACA	P35141	staphylococ
153	3	10.0	40	1	PHRK_BACSU	O31840	bacillus su
154	3	10.0	40	1	PRE_BACLI	P18189	bacillus li
155	3	10.0	40	1	RK33_PEA	P51416	pisum sativ
156	3	10.0	40	1	RRPO_LSV	P27328	lily sympto
157	3	10.0	40	1	SAUV_PHYSA	P01144	phyllomedus
158	3	10.0	40	1	SR1D_SARPE	P18312	sarcophaga
159	3	10.0	40	1	UC11_MAIZE	P80617	zea mays (m
160	3	10.0	40	1	VIT_MELGA	P56531	meleagris g
161	3	10.0	40	1	YDRB_STRPE	P32012	streptomyce
162	2	6.7	28	1	ACON_CANAL	P82611	candida alb
163	2	6.7	28	1	APC1_RABIT	P33047	oryctolagus
164	2	6.7	28	1	ARYC_NOCGL	P80008	nocardia gl
165	2	6.7	28	1	CIQC_RAT	P31722	rattus norv
166	2	6.7	28	1	ETX2_BACCE	P80568	bacillus ce
167	2	6.7	28	1	FIBA_CANFA	P02673	canis famil
168	2	6.7	28	1	FLA1_TREPH	P21988	treponema p
169	2	6.7	28	1	GDO_TRIMO	P02865	triticum mo
170	2	6.7	28	1	GRP_ALLMI	P31886	alligator m
171	2	6.7	28	1	GTS5_CHICK	P20137	gallus gall
172	2	6.7	28	1	GVPC_OSCAG	P80999	oscillatori
173	2	6.7	28	1	HORC_HORSP	P02864	hordeum spo
174	2	6.7	28	1	ICPP_VIPLE	P82475	vipera lebe
175	2	6.7	28	1	IEL1_MOMCH	P10296	momordica c
176	2	6.7	28	1	IORB_METTM	P80911	methanobact
177	2	6.7	28	1	ITR2_MOMCH	P10295	momordica c
178	2	6.7	28	1	ITR3_LUFCY	P35628	luffa cylin
179	2	6.7	28	1	ITRA_MOMCH	P30709	momordica c
180	2	6.7	28	1	LECA_IRIHO	P36230	iris hollan
181	2	6.7	28	1	LPFS_ECOLI	P22183	escherichia
182	2	6.7	28	1	LPL_ECOLI	P09149	escherichia
183	2	6.7	28	1	LPL_SALTI	Q8z9h9	salmonella
184	2	6.7	28	1	LPL_SALTY	P03062	salmonella
185	2	6.7	28	1	LPW_SERMA	P03055	serratia ma
186	2	6.7	28	1	MAAI_RAT	P57113	rattus norv
187	2	6.7	28	1	MCDP_MEGPE	P04567	megabombus
188	2	6.7	28	1	NLT2_WHEAT	P39085	triticum ae

189	2	6.7	28	1	NXL1_BOUAN	P34074	boulengerin
190	2	6.7	28	1	OBP1_HYSCR	P81647	hystrix cri
191	2	6.7	28	1	OMPA_YERPS	P38399	yersinia ps
192	2	6.7	28	1	ORND_PLAOR	P25513	placobdella
193	2	6.7	28	1	OST1_CHICK	P80896	gallus gall
194	2	6.7	28	1	PA22_MICNI	P21791	micrurus ni
195	2	6.7	28	1	PA23_MICNI	P21792	micrurus ni
196	2	6.7	28	1	PETL_CYAPA	P48102	cyanophora
197	2	6.7	28	1	PHR_METTM	P58818	methanobact
198	2	6.7	28	1	PHYB_ASPFI	P81440	aspergillus
199	2	6.7	28	1	PP71_HCMVT	P24429	human cytom
200	2	6.7	28	1	PPOX_BOVIN	P56602	bos taurus
201	2	6.7	28	1	RL5_HALCU	P05972	halobacteri
202	2	6.7	28	1	RS19_PHYS1	O66093	phytoplasma
203	2	6.7	28	1	SCX2_BUTSI	P15230	buthus sind
204	2	6.7	28	1	SLP1_LEIQH	P80669	leiurus qui
205	2	6.7	28	1	SMS2_ORENI	P81029	oreochromis
206	2	6.7	28	1	TXO2_AGEAP	P15971	agelenopsis
207	2	6.7	28	1	VG9_SPV4	P11341	spiroplasma
208	2	6.7	28	1	VIP_DIDMA	P39089	didelphis m
209	2	6.7	28	1	VIP_SCYCA	P09685	scyliorhinu
210	2	6.7	28	1	Y073_ARCFU	O30163	archaeoglob
211	2	6.7	28	1	Y16P_BPT4	P39248	bacterioph
212	2	6.7	28	1	YA79_ARCFU	O29184	archaeoglob
213	2	6.7	29	1	12AH_CLOS4	P21215	clostridium
214	2	6.7	29	1	AL21_HORSE	P81216	equis cabal
215	2	6.7	29	1	ATP9_PICPJ	Q06838	pichia pijp
216	2	6.7	29	1	ATPA_BRYMA	P26965	bryopsis ma
217	2	6.7	29	1	BR2D_RANES	P40840	rana escule
218	2	6.7	29	1	BREE_RANES	P40841	rana escule
219	2	6.7	29	1	CERB_CERCA	P36191	ceratitis c
220	2	6.7	29	1	COA1_BPI22	P15413	bacterioph
221	2	6.7	29	1	COXJ_CANFA	Q9tr29	canis famil
222	2	6.7	29	1	COXK_SHEEP	Q9tr28	ovis aries
223	2	6.7	29	1	CU36_LOCFI	P11737	locusta mig
224	2	6.7	29	1	CXD6_CONGL	Q9twm7	conus glori
225	2	6.7	29	1	CXOC_CONMA	P37300	conus magus
226	2	6.7	29	1	CXOD_CONMA	Q26350	conus magus
227	2	6.7	29	1	CXST_CONGE	P58844	conus geogr
228	2	6.7	29	1	DMS5_PHYSA	P80281	phyllomedus
229	2	6.7	29	1	GLUC_ANAPL	P01276	anas platyr
230	2	6.7	29	1	GLUC_CALMI	P13189	callorhynch
231	2	6.7	29	1	GLUC_DIDMA	P18108	didelphis m
232	2	6.7	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
233	2	6.7	29	1	GLUC_PLAFE	P23062	platichthys
234	2	6.7	29	1	GLUC_RABIT	P25449	oryctolagus
235	2	6.7	29	1	GLUC_TORMA	P09567	torpedo mar
236	2	6.7	29	1	H2B2_ECHES	P13282	echinus esc
237	2	6.7	29	1	HOXY_RHOOP	P22660	rhodococcus
238	2	6.7	29	1	HRJ_BOTJA	P20416	bothrops ja
239	2	6.7	29	1	HS98_NEUCR	P31540	neurospora
240	2	6.7	29	1	ITH3_BOVIN	P56652	bos taurus
241	2	6.7	29	1	ITR1_CUCMA	P01074	cucurbita m
242	2	6.7	29	1	ITR1_LUFCY	P25849	luffa cylin
243	2	6.7	29	1	ITR1_MOMRE	P17680	momordica r
244	2	6.7	29	1	ITR2_BRYDI	P11968	bryonia dio
245	2	6.7	29	1	ITR3_CYCPE	P83394	cyclanthera

246	2	6.7	29	1	ITR4_CYCPE	P83395	cyclanthera
247	2	6.7	29	1	ITR5_CYCPE	P83396	cyclanthera
248	2	6.7	29	1	KDPF_ECOLI	P36937	escherichia
249	2	6.7	29	1	MDH_BURPS	P80536	burkholderi
250	2	6.7	29	1	MULR_ECHML	P81798	echis multi
251	2	6.7	29	1	PETN_ANASP	Q913p6	anabaena sp
252	2	6.7	29	1	PETN_ARATH	P12178	arabidopsis
253	2	6.7	29	1	PETN_CHAGL	Q8ma13	chaetosphae
254	2	6.7	29	1	PETN_CYAPA	P48258	cyanophora
255	2	6.7	29	1	PETN_GUITH	O78498	guillardia
256	2	6.7	29	1	PETN_MAIZE	Q33302	zea mays (m
257	2	6.7	29	1	PETN_MARPO	P12177	marchantia
258	2	6.7	29	1	PETN_MESVI	Q9mus4	mesostigma
259	2	6.7	29	1	PETN_ODOSI	P49527	odontella s
260	2	6.7	29	1	PETN_PINTH	P41611	pinus thunb
261	2	6.7	29	1	PETN_PORPU	P51276	porphyra pu
262	2	6.7	29	1	PETN_PSINU	Q8wi23	psilotum nu
263	2	6.7	29	1	PETN_SKECO	O96807	skeletonema
264	2	6.7	29	1	PETN_SYNEL	Q8dkn2	synechococc
265	2	6.7	29	1	PETN_SYNY3	P72717	synechocyst
266	2	6.7	29	1	PK4_DICDI	P34103	dictyosteli
267	2	6.7	29	1	PRO1_DACGL	P18689	dactylis gl
268	2	6.7	29	1	PSAF_SYNP6	P31083	synechococc
269	2	6.7	29	1	PSAK_SPIOL	P14627	spinacia ol
270	2	6.7	29	1	PSAM_GUITH	O78448	guillardia
271	2	6.7	29	1	PSBI_SYNVU	P12240	synechococc
272	2	6.7	29	1	RL15_HALCU	P05971	halobacteri
273	2	6.7	29	1	RL15_STRLI	P49975	streptomyce
274	2	6.7	29	1	RP54_CLOKL	P38944	clostridium
275	2	6.7	29	1	SCX1_ANDMA	P56215	androctonus
276	2	6.7	29	1	SDHB_CLOPR	P80213	clostridium
277	2	6.7	29	1	SLP2_LEIQH	P80670	leiurus qui
278	2	6.7	29	1	SLP3_LEIQH	P80671	leiurus qui
279	2	6.7	29	1	TAT_HV1Z3	P12510	human immun
280	2	6.7	29	1	TLP_ACTDE	P81370	actinidia d
281	2	6.7	29	1	VARF_VIOAR	P58451	viola arven
282	2	6.7	29	1	Y15_BPT7	P03792	bacterioph
283	2	6.7	29	1	Y51_BPT3	P20326	bacterioph
284	2	6.7	29	1	YCX4_ODOSI	P49830	odontella s
285	2	6.7	29	1	YCX4_ODOSI	P49838	odontella s
286	2	6.7	30	1	2ENR_CLOTY	P11887	clostridium
287	2	6.7	30	1	A1AT_CHIVI	P38026	chinchilla
288	2	6.7	30	1	AATC_RABIT	P12343	oryctolagus
289	2	6.7	30	1	AATM_RABIT	P12345	oryctolagus
290	2	6.7	30	1	ACB1_DIGLA	P81624	digitalis l
291	2	6.7	30	1	AMPT_BACST	P00728	bacillus st
292	2	6.7	30	1	ANF_RANRI	P09196	rana ridibu
293	2	6.7	30	1	CALM_LYTPI	P05935	lytechinus
294	2	6.7	30	1	CBAL_BACST	P13722	bacillus st
295	2	6.7	30	1	CH60_CLOPA	P81339	clostridium
296	2	6.7	30	1	CIRA_CHAPA	P56871	chassalia p
297	2	6.7	30	1	CLPA_PINPS	P81671	pinus pinas
298	2	6.7	30	1	COAE_CORAM	P58101	corynebacte
299	2	6.7	30	1	COXC_SOLTU	P80500	solanum tub
300	2	6.7	30	1	CRG2_SCOWA	P19865	scoliodon w
301	2	6.7	30	1	CX2A_CONBE	P58625	conus betul
302	2	6.7	30	1	CX7A_CONTU	P58923	conus tulip

303	2	6.7	30	1	CXEX_CONCN	P58928	conus conso
304	2	6.7	30	1	CXK4_CONST	P58921	conus stria
305	2	6.7	30	1	CXVB_CONER	P58783	conus ermin
306	2	6.7	30	1	CY35_DESAC	P81079	desulfuromo
307	2	6.7	30	1	CY01_VIOOD	P82230	viola odora
308	2	6.7	30	1	CY08_VIOOD	P58440	viola odora
309	2	6.7	30	1	DEF2_MACMU	P82317	macaca mula
310	2	6.7	30	1	DIDH_COMTE	P80702	comamonas t
311	2	6.7	30	1	DIU2_HYLLI	P82015	hyles linea
312	2	6.7	30	1	DIU2_MANSE	P24858	manduca sex
313	2	6.7	30	1	END2_ONCKE	P01205	oncorhynchu
314	2	6.7	30	1	FIBR_PANIN	P22775	panulirus i
315	2	6.7	30	1	HCY2_HOMAM	P82297	homarus ame
316	2	6.7	30	1	HETA_RADMA	P58691	radianthus
317	2	6.7	30	1	HYPH_HYBPA	P58445	hybanthus p
318	2	6.7	30	1	IHFB_RHILE	P80606	rhizobium l
319	2	6.7	30	1	ITI1_LAGLE	P26771	lagenaria l
320	2	6.7	30	1	ITR1_CITLA	P11969	citrullus l
321	2	6.7	30	1	ITR1_MOMCH	P10294	momordica c
322	2	6.7	30	1	ITR2_ECBEL	P12071	ecballium e
323	2	6.7	30	1	ITR2_LUFCY	P25850	luffa cylin
324	2	6.7	30	1	ITR3_CUCMC	P32041	cucumis mel
325	2	6.7	30	1	ITR3_MOMCO	P82410	momordica c
326	2	6.7	30	1	ITR4_CUCSA	P10292	cucumis sat
327	2	6.7	30	1	ITR6_CYCPE	P83397	cyclanthera
328	2	6.7	30	1	ITR7_CYCPE	P83398	cyclanthera
329	2	6.7	30	1	KAB5_OLDAF	P58456	oldenlandia
330	2	6.7	30	1	LAS1_PIG	P80171	sus scrofa
331	2	6.7	30	1	LEAH_PHAVU	P81870	phaseolus v
332	2	6.7	30	1	MDH_HELGE	P80037	heliobacter
333	2	6.7	30	1	MMAL_DERMI	P16312	dermatophag
334	2	6.7	30	1	NU5M_PISOC	P24999	pisaster oc
335	2	6.7	30	1	NUO2_SOLTU	P80268	solanum tub
336	2	6.7	30	1	P2CO_ARTSP	P37365	arthrobacte
337	2	6.7	30	1	PCCA_MYXXA	P81185	myxococcus
338	2	6.7	30	1	PCG1_PACGO	P82414	pachycondyl
339	2	6.7	30	1	PCG5_PACGO	P82418	pachycondyl
340	2	6.7	30	1	PETN_NEPOL	Q9tl01	nephroselmi
341	2	6.7	30	1	PLF4_RABIT	P83470	oryctolagus
342	2	6.7	30	1	PLMS_SQUAC	P82542	squalus aca
343	2	6.7	30	1	PMGY_CANAL	P82612	candida alb
344	2	6.7	30	1	PRT1_CLUPA	P02335	clupea pall
345	2	6.7	30	1	PRT2_ONCMY	P02331	oncorhynchu
346	2	6.7	30	1	PRT3_ONCMY	P02332	oncorhynchu
347	2	6.7	30	1	PRT4_ONCMY	P02333	oncorhynchu
348	2	6.7	30	1	PRTB_ONCMY	P12819	oncorhynchu
349	2	6.7	30	1	PSAM_CYACA	Q9tlx5	cyanidium c
350	2	6.7	30	1	PSAM_MESVI	Q9mus2	mesostigma
351	2	6.7	30	1	PSAM_ODOSI	P49487	odontella s
352	2	6.7	30	1	PSAM_PINTH	P41601	pinus thunb
353	2	6.7	30	1	PYSD_METBA	P80524	methanosarc
354	2	6.7	30	1	RIPS_MOMCO	P20655	momordica c
355	2	6.7	30	1	RKGG_LEPKE	P21587	lepidochely
356	2	6.7	30	1	RNP_ODOVI	P19640	odocoileus
357	2	6.7	30	1	SCK2_TITSE	P08816	tityus serr
358	2	6.7	30	1	SCX2_CENLI	P18927	centruroide
359	2	6.7	30	1	SILU_RHIPU	P02885	rhizomucor

360	2	6.7	30	1	TAT_HV1ZH	P12512	human immun
361	2	6.7	30	1	TL1X_SPIOL	P82537	spinacia ol
362	2	6.7	30	1	TL29_SPIOL	P81833	spinacia ol
363	2	6.7	30	1	TX2_HETVE	P58426	heteropoda
364	2	6.7	30	1	UC35_MAIZE	P80641	zea mays (m
365	2	6.7	30	1	UDDP_SULAC	P80143	sulfolobus
366	2	6.7	30	1	URE1_ECOLI	Q03284	escherichia
367	2	6.7	30	1	VAA1_EQUAR	Q04236	equisetum a
368	2	6.7	30	1	VAA1_PSINU	Q04237	psilotum nu
369	2	6.7	30	1	VAA2_PSINU	Q04239	psilotum nu
370	2	6.7	30	1	VATN_BOVIN	P81134	bos taurus
371	2	6.7	30	1	VG03_BPPF1	P25137	bacterioph
372	2	6.7	30	1	VPU_HV1SC	P05948	human immun
373	2	6.7	30	1	VTTA_BPT3	P20837	bacterioph
374	2	6.7	30	1	Y161_TREPA	O83196	treponema p
375	2	6.7	30	1	Y357_BORBU	O51332	borrelia bu
376	2	6.7	30	1	Y425_BORBU	O51386	borrelia bu
377	2	6.7	30	1	Y573_TREPA	O83583	treponema p
378	2	6.7	30	1	Y932_TREPA	O83902	treponema p
379	2	6.7	30	1	YCCB_ECOLI	P24244	escherichia
380	2	6.7	31	1	A98A_DROME	O46201	drosophila
381	2	6.7	31	1	BCAM_PIG	O19098	sus scrofa
382	2	6.7	31	1	CIRB_CHAPA	P56879	chassalia p
383	2	6.7	31	1	COG5_BOVIN	P83437	bos taurus
384	2	6.7	31	1	COX4_NEUCR	P06809	neurospora
385	2	6.7	31	1	CTRP_PENMO	P35002	penaeus mon
386	2	6.7	31	1	CU54_LOCFI	P11738	locusta mig
387	2	6.7	31	1	CXD6_CONNI	P56710	conus nigro
388	2	6.7	31	1	CXG6_CONTE	P58922	conus texti
389	2	6.7	31	1	CYLA_PSYLO	P56872	psychotria
390	2	6.7	31	1	DEF2_MESAU	P81466	mesocricetu
391	2	6.7	31	1	EFTU_STRLU	P52390	streptomyce
392	2	6.7	31	1	ENDB_CAMDR	P01203	camelus dro
393	2	6.7	31	1	ER29_BOVIN	P81623	bos taurus
394	2	6.7	31	1	ETFD_PARDE	P55932	paracoccus
395	2	6.7	31	1	FIBB_CANFA	P02677	canis famil
396	2	6.7	31	1	GT_SERMA	P22416	serratia ma
397	2	6.7	31	1	HBA_MACEU	P81043	macropus eu
398	2	6.7	31	1	HCY1_HOMAM	P82296	homarus ame
399	2	6.7	31	1	HCY2_MAISQ	P82303	maia squina
400	2	6.7	31	1	HEM2_PHAGO	P27687	phascolopsi
401	2	6.7	31	1	LC70_LACPA	P80959	lactobacill
402	2	6.7	31	1	LCCB_LEUME	P81052	leuconostoc
403	2	6.7	31	1	LPRM_ECOLI	P10739	escherichia
404	2	6.7	31	1	MDH_STRAR	P19982	streptomyce
405	2	6.7	31	1	PETL_ANASP	Q8yvq2	anabaena sp
406	2	6.7	31	1	PETL_ARATH	P56776	arabidopsis
407	2	6.7	31	1	PETL_BETVU	P46612	beta vulgar
408	2	6.7	31	1	PETL_CHLVU	P56306	chlorella v
409	2	6.7	31	1	PETL_GUIITH	O78468	guillardia
410	2	6.7	31	1	PETL_MAIZE	P19445	zea mays (m
411	2	6.7	31	1	PETL_ODOSI	P49524	odontella s
412	2	6.7	31	1	PETL_OENHO	Q9mtk4	oenothera h
413	2	6.7	31	1	PETL_ORYSA	P12180	oryza sativ
414	2	6.7	31	1	PETL_PORPU	P51221	porphyra pu
415	2	6.7	31	1	PETL_PSINU	Q8wi03	psilotum nu
416	2	6.7	31	1	PETL_SPIOL	Q9m310	spinacia ol

417	2	6.7	31	1	PETL_WHEAT	P58247	triticum ae
418	2	6.7	31	1	PETM_CYACA	Q9t1r5	cyanidium c
419	2	6.7	31	1	PETN_CYACA	Q9t1r6	cyanidium c
420	2	6.7	31	1	PRT2_CLUPA	P02336	clupea pall
421	2	6.7	31	1	PSAK_ANAVA	P23317	anabaena va
422	2	6.7	31	1	PSAM_CHLVU	P56314	chlorella v
423	2	6.7	31	1	PSAM_CYAPA	P48185	cyanophora
424	2	6.7	31	1	PSBK_SYNVU	P19054	synechococc
425	2	6.7	31	1	PSBM_MESVI	Q9muq7	mesostigma
426	2	6.7	31	1	PSBT_CHLRE	P37256	chlamydomon
427	2	6.7	31	1	PSBT_CHLVU	P56327	chlorella v
428	2	6.7	31	1	PSBT_CYAPA	P48109	cyanophora
429	2	6.7	31	1	PSBT_EUGGR	P20176	euglena gra
430	2	6.7	31	1	PSBT_MESVI	Q9muv6	mesostigma
431	2	6.7	31	1	PSBT_PORPU	P51323	porphyra pu
432	2	6.7	31	1	PYSG_METBA	P80523	methanosarc
433	2	6.7	31	1	RECX_METCL	P37865	methylomona
434	2	6.7	31	1	RL21_STRTR	P48956	streptococc
435	2	6.7	31	1	SARL_HUMAN	O00631	homo sapien
436	2	6.7	31	1	SC37_MESMA	P83407	mesobuthus
437	2	6.7	31	1	SODC_STRHE	P81163	striga herm
438	2	6.7	31	1	TX3_HETVE	P58427	heteropoda
439	2	6.7	31	1	TXA3_PARAC	P09949	parasicyoni
440	2	6.7	31	1	Y191_BORBU	O51209	borrelia bu
441	2	6.7	31	1	Y3KD_BPCHP	P19187	bacterioph
442	2	6.7	31	1	Y603_ARCFU	O29652	archaeoglob
443	2	6.7	32	1	A2M_PACLE	P20738	pacifastacu
444	2	6.7	32	1	APL3_DIAGR	P81471	diatraea gr
445	2	6.7	32	1	ATP0_PIG	P80021	sus scrofa
446	2	6.7	32	1	ATP7_SPIOL	P80088	spinacia ol
447	2	6.7	32	1	ATP0_SPIOL	P80087	spinacia ol
448	2	6.7	32	1	B4G1_RAT	P80225	r beta-1,4-
449	2	6.7	32	1	CAAP_MICEC	P21162	micromonosp
450	2	6.7	32	1	CAL0_BOVIN	P01260	bos taurus
451	2	6.7	32	1	CAL0_PIG	P01259	sus scrofa
452	2	6.7	32	1	CAR1_ECHCA	Q9prp9	echis carin
453	2	6.7	32	1	CEC_OIKKI	P83420	oiketicus k
454	2	6.7	32	1	COA1_BPIF1	O80295	bacterioph
455	2	6.7	32	1	COA1_BPIKE	P03676	bacterioph
456	2	6.7	32	1	COA2_BPFD	P03677	bacterioph
457	2	6.7	32	1	CRP_PLEPL	P12245	pleuronecte
458	2	6.7	32	1	CXG7_CONPE	P56711	conus penna
459	2	6.7	32	1	CYBL_RHOGR	P32953	rhodotorula
460	2	6.7	32	1	CYSB_FASHE	P80529	fasciola he
461	2	6.7	32	1	DBH_SYNY1	P02343	synechocyst
462	2	6.7	32	1	ER29_CHICK	P81628	gallus gall
463	2	6.7	32	1	ER29_TRIVU	P81629	trichosurus
464	2	6.7	32	1	ERH_PIG	P80230	sus scrofa
465	2	6.7	32	1	FER_PORCR	P18821	porphyridiu
466	2	6.7	32	1	FLA1_METHU	P17603	methanospir
467	2	6.7	32	1	FRIH_ANAPL	P80145	anas platyr
468	2	6.7	32	1	GHR4_RAT	P33581	rattus norv
469	2	6.7	32	1	GLB4_LAMSP	P20413	lamellibrac
470	2	6.7	32	1	GT82_DICLA	P82608	dicentrarch
471	2	6.7	32	1	H2AZ_ONCMY	P22647	oncorhynch
472	2	6.7	32	1	HCCY_CHEDE	P83172	cherax dest
473	2	6.7	32	1	IAPP_BOVIN	Q28207	bos taurus

474	2	6.7	32	1	IAPP_SAGOE	Q28934	saguinus oe
475	2	6.7	32	1	IAPP_SHEEP	Q28605	ovis aries
476	2	6.7	32	1	ILVB_ENTAE	Q09129	enterobacte
477	2	6.7	32	1	ITR2_CUCSA	P10291	cucumis sat
478	2	6.7	32	1	LPID_ECOLI	P03060	escherichia
479	2	6.7	32	1	LPID_EDWTA	P08140	edwardsiell
480	2	6.7	32	1	LPIV_ECOLI	P03061	escherichia
481	2	6.7	32	1	MDH_NITAL	P10887	nitzschia a
482	2	6.7	32	1	NEUB_PIG	P01297	sus scrofa
483	2	6.7	32	1	OVOS_ANAPL	P20739	anas platyr
484	2	6.7	32	1	PA22_AGKHP	P18997	agkistrodon
485	2	6.7	32	1	PA2_RHONO	P43318	rhophilema n
486	2	6.7	32	1	PETL_CHLRE	P50369	chlamydomon
487	2	6.7	32	1	PETM_PORPU	P51275	porphyra pu
488	2	6.7	32	1	PHNS_DESMU	P13062	desulfovibr
489	2	6.7	32	1	PRI3_ONCMY	P02330	oncorhynchu
490	2	6.7	32	1	PRT1_ONCKE	P02327	oncorhynchu
491	2	6.7	32	1	PRT4_SCYCA	P30259	scyliorhinu
492	2	6.7	32	1	PRT5_ONCMY	P02334	oncorhynchu
493	2	6.7	32	1	PRT6_ONCMY	P08145	oncorhynchu
494	2	6.7	32	1	PRT7_ONCMY	P08146	oncorhynchu
495	2	6.7	32	1	PRT8_ONCMY	P12817	oncorhynchu
496	2	6.7	32	1	PRT9_ONCMY	P08147	oncorhynchu
497	2	6.7	32	1	PRTA_ONCMY	P12818	oncorhynchu
498	2	6.7	32	1	PRT_ORYLA	Q91185	oryzias lat
499	2	6.7	32	1	PSBT_CYACA	O19927	cyanidium c
500	2	6.7	32	1	PSBT_GUITH	O78512	guillardia
501	2	6.7	32	1	PSBZ_EUGAN	Q8s195	euglena ana
502	2	6.7	32	1	PSBZ_EUGMY	Q8s191	euglena myx
503	2	6.7	32	1	RIP2_PHYDI	P34967	phytolacca
504	2	6.7	32	1	RK1_RABIT	P81655	oryctolagus
505	2	6.7	32	1	RS19_YEREN	Q56847	yersinia en
506	2	6.7	32	1	SCK2_CENNO	P58504	centruroide
507	2	6.7	32	1	TAT_SIVM2	P05912	simian immu
508	2	6.7	32	1	TRYP_PENMO	P35050	penaeus mon
509	2	6.7	32	1	TX29_PHONI	P29426	phoneutria
510	2	6.7	32	1	TXP7_APTSC	P49271	aptostichus
511	2	6.7	32	1	UC09_MAIZE	P80615	zea mays (m
512	2	6.7	32	1	Y169_TREPA	O83199	treponema p
513	2	6.7	32	1	Y433_BORBU	O51394	borrelia bu
514	2	6.7	32	1	YH17_HAEIN	P44295	haemophilus
515	2	6.7	32	1	YSCA_YEREN	Q01242	yersinia en
516	2	6.7	32	1	YTK3_ILTVT	P23985	infectious
517	2	6.7	33	1	ACT_DICVI	Q24733	dictyocaulu
518	2	6.7	33	1	ALOX_PICPA	P04842	pichia past
519	2	6.7	33	1	ANP3_MYOSC	P04367	myoxocephal
520	2	6.7	33	1	ANP5_MYOAE	P20421	myoxocephal
521	2	6.7	33	1	ATP7_SOLTU	P80496	solanum tub
522	2	6.7	33	1	BR2A_RANES	P40837	rana escule
523	2	6.7	33	1	BR2B_RANES	P40838	rana escule
524	2	6.7	33	1	BR2E_RANES	P32413	rana escule
525	2	6.7	33	1	BR2_RANBP	P32424	rana brevip
526	2	6.7	33	1	CECB_HELVI	P83414	heliiothis v
527	2	6.7	33	1	CECC_HELVI	P83415	heliiothis v
528	2	6.7	33	1	COA1_BPFD	P03675	bacterioph
529	2	6.7	33	1	COA2_BPI22	P15414	bacterioph
530	2	6.7	33	1	COA2_BPIKE	P03678	bacterioph

531	2	6.7	33	1	COXL_ONCMY	P80330	oncorhynchu
532	2	6.7	33	1	CU89_HUMAN	P59042	homo sapien
533	2	6.7	33	1	CXBW_CONRA	P58804	conus radia
534	2	6.7	33	1	CXO_CONVE	P83301	conus ventr
535	2	6.7	33	1	DBB2_DOLAU	P83376	dolabella a
536	2	6.7	33	1	DEF1_MESAU	P81465	mesocricetu
537	2	6.7	33	1	DEF3_MESAU	P81467	mesocricetu
538	2	6.7	33	1	DEF4_MESAU	P81468	mesocricetu
539	2	6.7	33	1	DHE3_PIG	P42174	sus scrofa
540	2	6.7	33	1	FER_PORAE	P18820	porphyridiu
541	2	6.7	33	1	GAST_CAVPO	P06885	cavia porce
542	2	6.7	33	1	GAST_CHIBR	P10034	chinchilla
543	2	6.7	33	1	GAST_DIDMA	P33713	didelphis m
544	2	6.7	33	1	GGN2_RANRU	P80396	rana rugosa
545	2	6.7	33	1	GGN3_RANRU	P80397	rana rugosa
546	2	6.7	33	1	HF40_MAIZE	P82865	zea mays (m
547	2	6.7	33	1	HOXU_RHOOP	P22659	rhodococcus
548	2	6.7	33	1	LPPY_SALTY	P08522	salmonella
549	2	6.7	33	1	LPRH_ECOLI	P37324	escherichia
550	2	6.7	33	1	LYC2_HORSE	P81710	equus cabal
551	2	6.7	33	1	MBP1_MAIZE	P28794	zea mays (m
552	2	6.7	33	1	MHAA_STRCH	P80435	streptomyce
553	2	6.7	33	1	MYMY_MYTED	P81614	mytilus edu
554	2	6.7	33	1	OTCC_PSEPU	P11727	pseudomonas
555	2	6.7	33	1	PEN3_ADECU	P35987	canine aden
556	2	6.7	33	1	PETM_CYAPA	P48366	cyanophora
557	2	6.7	33	1	PETM_SYNEL	Q8dj15	synechococc
558	2	6.7	33	1	PK1_DICDI	P34101	dictyosteli
559	2	6.7	33	1	PK5_DICDI	P34104	dictyosteli
560	2	6.7	33	1	PRI1_ONCMY	P02326	oncorhynchu
561	2	6.7	33	1	PRI2_ONCMY	P02328	oncorhynchu
562	2	6.7	33	1	PRTB_MUGCE	P08130	mugil cepha
563	2	6.7	33	1	PRTL_ECOLI	P02338	escherichia
564	2	6.7	33	1	PSAK_CUCSA	P42051	cucumis sat
565	2	6.7	33	1	PSBT_ARATH	P37259	arabidopsis
566	2	6.7	33	1	PSBT_MAIZE	P37257	zea mays (m
567	2	6.7	33	1	RL21_XENLA	P49628	xenopus lae
568	2	6.7	33	1	RL26_XENLA	P49629	xenopus lae
569	2	6.7	33	1	RL28_XENLA	P46780	xenopus lae
570	2	6.7	33	1	RL4_HALCU	P05967	halobacteri
571	2	6.7	33	1	RPOC_HETCA	P36441	heterosigma
572	2	6.7	33	1	RRPO_BPBZ1	P09674	bacterioph
573	2	6.7	33	1	RS4_XENLA	P49401	xenopus lae
574	2	6.7	33	1	RT25_BOVIN	P82669	bos taurus
575	2	6.7	33	1	RUGA_RANRU	P80954	rana rugosa
576	2	6.7	33	1	SCX9_BUTO	P04099	buthus occi
577	2	6.7	33	1	THIO_CLOST	P81109	clostridium
578	2	6.7	33	1	TX1_HETVE	P58425	heteropoda
579	2	6.7	33	1	TXH1_SELHU	P56676	selenocosmi
580	2	6.7	33	1	TXN3_SELHA	P83464	selenocosmi
581	2	6.7	33	1	VT1B_RAT	P58200	rattus norv
582	2	6.7	33	1	Y474_BORBU	O51430	borrelia bu
583	2	6.7	33	1	Y656_TREPA	O83662	treponema p
584	2	6.7	33	1	Y849_BORBU	O51789	borrelia bu
585	2	6.7	33	1	YC12_CHLRE	P50370	chlamydomon
586	2	6.7	33	1	YC12_MARPO	P31560	marchantia
587	2	6.7	33	1	YC12_MESVI	Q9mus3	mesostigma

588	2	6.7	33	1	YC12_NEPOL	Q9tky6	nephroselmi
589	2	6.7	33	1	YC12_PINTH	P41600	pinus thunb
590	2	6.7	33	1	YL74_ARCFU	O28108	archaeoglob
591	2	6.7	33	1	YLCH_BP82	Q37869	bacterioph
592	2	6.7	33	1	YLCH_ECOLI	Q47268	escherichia
593	2	6.7	34	1	AMP2_CHICK	P80390	gallus gall
594	2	6.7	34	1	ASPG_PIG	P30918	sus scrofa
595	2	6.7	34	1	BR2C_RANES	P40839	rana escule
596	2	6.7	34	1	COL_CHICK	P11148	gallus gall
597	2	6.7	34	1	COXA_THETH	P82543	thermus the
598	2	6.7	34	1	COXG_THUOB	P80976	thunnus obe
599	2	6.7	34	1	CXGS_CONGE	P15472	conus geogr
600	2	6.7	34	1	DEF2_RABIT	P07468	oryctolagus
601	2	6.7	34	1	DEF7_RABIT	P80223	oryctolagus
602	2	6.7	34	1	ECAB_ECTTU	P49344	ectatomma t
603	2	6.7	34	1	EF2_RABIT	P55823	oryctolagus
604	2	6.7	34	1	EGGR_APLCA	P01363	aplysia cal
605	2	6.7	34	1	HIS_STRPU	P19376	strongyloce
606	2	6.7	34	1	HS7S_CUCMA	P31082	cucurbita m
607	2	6.7	34	1	ITR1_MOMCO	P82408	momordica c
608	2	6.7	34	1	ITR2_MOMCO	P82409	momordica c
609	2	6.7	34	1	LPTN_PROVU	P28779	proteus vul
610	2	6.7	34	1	M44E_HUMAN	Q96pg1	homo sapien
611	2	6.7	34	1	MYTB_MYTED	P81613	mytilus edu
612	2	6.7	34	1	PETM_ANASP	Q9f4w2	anabaena sp
613	2	6.7	34	1	PRT1_SAROR	P25327	sarda orien
614	2	6.7	34	1	PRT1_SCOSC	P83264	scomber sco
615	2	6.7	34	1	PRT1_THUTH	P02321	thunnus thy
616	2	6.7	34	1	PRT2_SCOSC	P83265	scomber sco
617	2	6.7	34	1	PRT2_THUTH	P02322	thunnus thy
618	2	6.7	34	1	PRT_DICLA	Q9ps27	dicentrarch
619	2	6.7	34	1	PRT_PERFV	P29629	perca flave
620	2	6.7	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
621	2	6.7	34	1	PSAI_OENHO	Q9mtl2	oenothera h
622	2	6.7	34	1	PSBM_ARATH	P12169	arabidopsis
623	2	6.7	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
624	2	6.7	34	1	PSBM_CHLRE	P92277	chlamydomon
625	2	6.7	34	1	PSBM_MAIZE	P48189	zea mays (m
626	2	6.7	34	1	PSBM_MARPO	P12168	marchantia
627	2	6.7	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
628	2	6.7	34	1	PSBM_OENHO	Q9mtm8	oenothera h
629	2	6.7	34	1	PSBM_PEA	P34833	pisum sativ
630	2	6.7	34	1	PSBM_PSINU	Q8wi22	psilotum nu
631	2	6.7	34	1	PSBM_WHEAT	Q9xps6	triticum ae
632	2	6.7	34	1	PSBT_TOBAC	P12184	nicotiana t
633	2	6.7	34	1	PSPC_BOVIN	P15783	bos taurus
634	2	6.7	34	1	PSPC_CANFA	P22397	canis famil
635	2	6.7	34	1	PYSB_METBA	P80522	methanosarc
636	2	6.7	34	1	RNL1_PIG	P15466	sus scrofa
637	2	6.7	34	1	RR2_OCHNE	Q40606	ochrosphaer
638	2	6.7	34	1	SCXM_SCOMA	P80719	scorpio mau
639	2	6.7	34	1	SMS_MYXGL	P19209	myxine glut
640	2	6.7	34	1	THEM_MALSU	P13858	malbranchea
641	2	6.7	34	1	TX33_PHONI	P81789	phoneutria
642	2	6.7	34	1	TXP5_BRASM	P49266	brachypelma
643	2	6.7	34	1	VLYS_BPM1	P08229	bacterioph
644	2	6.7	34	1	VPU_HV1W2	P08808	human immun

645	2	6.7	34	1	Y05J_BPT4	P39239	bacterioph
646	2	6.7	34	1	Y224_TREPA	O83253	treponema p
647	2	6.7	34	1	Y848_BORBU	O51788	borrelia bu
648	2	6.7	34	1	Y870_HAEIN	P44065	haemophilus
649	2	6.7	34	1	Y967_HAEIN	P44086	haemophilus
650	2	6.7	34	1	YC12_GUITH	O78460	guillardia
651	2	6.7	34	1	YC12_ODOSI	P49529	odontella s
652	2	6.7	34	1	YC12_PORPU	P51385	porphyra pu
653	2	6.7	34	1	YC12_SKECO	O96797	skeletonema
654	2	6.7	34	1	YMIA_AGR TU	P38437	agrobacteri
655	2	6.7	34	1	Z33B_HUMAN	Q06731	homo sapien
656	2	6.7	35	1	ADO1_AGRDO	P58608	agriosphodr
657	2	6.7	35	1	C550_BACHA	P80091	bacillus ha
658	2	6.7	35	1	CEC4_BOMMO	P14666	bombyx mori
659	2	6.7	35	1	CECA_HELVI	P83413	heliiothis v
660	2	6.7	35	1	CECB_ANTPE	P01509	antheraea p
661	2	6.7	35	1	D3HI_RABIT	P32185	oryctolagus
662	2	6.7	35	1	DEFB_MYTED	P81611	mytilus edu
663	2	6.7	35	1	END4_YEREN	P42691	yersinia en
664	2	6.7	35	1	ERFK_KLEAE	Q08599	klebsiella
665	2	6.7	35	1	EXE2_HEL SU	P04204	heloderma s
666	2	6.7	35	1	FAS_CAPHI	P08757	capra hircu
667	2	6.7	35	1	FLAV_NOSSM	P35707	nostoc sp.
668	2	6.7	35	1	GBGU_MOUSE	Q61017	mus musculu
669	2	6.7	35	1	GRDB_CLOPU	P55793	clostridium
670	2	6.7	35	1	GUR_GYMSY	P25810	gymnema syl
671	2	6.7	35	1	HMWC_DESGI	P38588	desulfovibr
672	2	6.7	35	1	IAAC_HORVU	P34951	hordeum vul
673	2	6.7	35	1	KPPR_PINPS	P81664	pinus pinas
674	2	6.7	35	1	LCGB_LACLA	P36962	lactococcus
675	2	6.7	35	1	NEF_HV1H3	P05854	human immun
676	2	6.7	35	1	PBP1_LYMDI	P34176	lymantria d
677	2	6.7	35	1	PBP2_LYMDI	P34177	lymantria d
678	2	6.7	35	1	PBP_HYACE	P34175	hyalophora
679	2	6.7	35	1	PHI1_MYTCA	P35422	mytilus cal
680	2	6.7	35	1	PSAI_CYAPA	P48116	cyanophora
681	2	6.7	35	1	PSBT_MARPO	P12182	marchantia
682	2	6.7	35	1	PSBT_OENHO	P37258	oenothera h
683	2	6.7	35	1	PSBT_ORYSA	P12183	oryza sativ
684	2	6.7	35	1	PSBT_PINTH	P41625	pinus thunb
685	2	6.7	35	1	PSPC_PIG	P15785	sus scrofa
686	2	6.7	35	1	RL32_HALCU	P05965	halobacteri
687	2	6.7	35	1	SCKB_PANIM	P55928	pandinus im
688	2	6.7	35	1	SCKG_PANIM	Q10726	pandinus im
689	2	6.7	35	1	SCX1_BUTSI	P15229	buthus sind
690	2	6.7	35	1	SCX5_BUTEU	P15222	buthus eupe
691	2	6.7	35	1	SCXP_ANDMA	P01498	androctonus
692	2	6.7	35	1	SMS_LAMFL	Q9prro	lampetra fl
693	2	6.7	35	1	SPRC_PIG	P20112	sus scrofa
694	2	6.7	35	1	THPA_THADA	P21381	thaumatococ
695	2	6.7	35	1	TMTX_MESTA	Q9bn12	mesobuthus
696	2	6.7	35	1	TXAG_AGEOP	P31328	agelena opu
697	2	6.7	35	1	TXH4_SELHU	P83303	selenocosmi
698	2	6.7	35	1	TXKS_STOHE	P29187	stoichactis
699	2	6.7	35	1	TXN4_SELHA	P83471	selenocosmi
700	2	6.7	35	1	VL3_PAPVD	P06919	deer papill
701	2	6.7	35	1	VSPA_CERVI	P18692	cerastes vi

702	2	6.7	35	1	WSP7_PINPS	P81086	pinus pinas
703	2	6.7	35	1	Y210_HAEIN	P43964	haemophilus
704	2	6.7	35	1	Y320_BORBU	O51299	borrelia bu
705	2	6.7	35	1	Y37_BPT3	P20325	bacterioph
706	2	6.7	35	1	Y644_ARCFU	O29613	archaeoglob
707	2	6.7	35	1	Y845_BORBU	O51785	borrelia bu
708	2	6.7	35	1	Y847_BORBU	O51787	borrelia bu
709	2	6.7	35	1	YC12_CYACA	Q9tlx0	cyanidium c
710	2	6.7	35	1	YC69_ARCFU	O28999	archaeoglob
711	2	6.7	35	1	YQB5_CAEEL	Q09258	caenorhabdi
712	2	6.7	36	1	AMPL_PIG	P28839	sus scrofa
713	2	6.7	36	1	ANFV_ANGJA	P22642	anguilla ja
714	2	6.7	36	1	C3L1_BOVIN	P30922	bos taurus
715	2	6.7	36	1	CBBA_NITVU	P37102	nitrobacter
716	2	6.7	36	1	CECD_ANTPE	P01511	antheraea p
717	2	6.7	36	1	CYC7_GEOME	P81894	geobacter m
718	2	6.7	36	1	F4RE_METOG	P80951	methanogeni
719	2	6.7	36	1	GLU1_ORENI	P81026	oreochromis
720	2	6.7	36	1	GLUC_HYDCO	P09682	hydrolagus
721	2	6.7	36	1	HIL5_ENSMI	P27203	ensis minor
722	2	6.7	36	1	HBB_PONPY	Q9tt34	pongo pygma
723	2	6.7	36	1	IAA_STRAU	P04082	streptomyce
724	2	6.7	36	1	IOB1_ISYOB	P58609	isyndus obs
725	2	6.7	36	1	KAD_STRGR	P53398	streptomyce
726	2	6.7	36	1	LHG_RHOVI	P04126	rhodopseudo
727	2	6.7	36	1	LYOX_PIG	P45845	sus scrofa
728	2	6.7	36	1	MFA1_YEAST	P34165	saccharomyc
729	2	6.7	36	1	MPG2_DACGL	Q41183	dactylis gl
730	2	6.7	36	1	MYPC_RAT	P56741	rattus norv
731	2	6.7	36	1	NEUH_CARCA	P11975	cardisoma c
732	2	6.7	36	1	NEUY_GADMO	P80167	gadus morhu
733	2	6.7	36	1	NEUY_ONCMY	P29071	oncorhynch
734	2	6.7	36	1	NEUY_RABIT	P09640	oryctolagus
735	2	6.7	36	1	NEUY_RANRI	P29949	rana ridibu
736	2	6.7	36	1	NIFH_ENTAG	P26249	enterobacte
737	2	6.7	36	1	NLTP_PINPI	P26912	pinus pinea
738	2	6.7	36	1	NUCM_SOLTU	P80264	solanum tub
739	2	6.7	36	1	OST2_CHICK	P80897	gallus gall
740	2	6.7	36	1	PAHO_ALLMI	P06305	alligator m
741	2	6.7	36	1	PAHO_ANSAN	P06304	anser anser
742	2	6.7	36	1	PAHO_CERSI	P37999	ceratotheri
743	2	6.7	36	1	PAHO_DIDMA	P18107	didelphis m
744	2	6.7	36	1	PAHO_EQUZE	P38000	equus zebra
745	2	6.7	36	1	PAHO_ERIEU	P41335	erinaceus e
746	2	6.7	36	1	PAHO_LARAR	P41337	larus argen
747	2	6.7	36	1	PAHO_MACMU	P33684	macaca mula
748	2	6.7	36	1	PAHO_RABIT	P41336	oryctolagus
749	2	6.7	36	1	PAHO_RANCA	P15427	rana catesb
750	2	6.7	36	1	PAHO_RANTE	P31229	rana tempor
751	2	6.7	36	1	PAHO_STRCA	P11967	struthio ca
752	2	6.7	36	1	PAHO_TAPPI	P39659	tapirus pin
753	2	6.7	36	1	PGKH_CHLFU	P36232	chlorella f
754	2	6.7	36	1	PMY_PETMA	P80024	petromyzon
755	2	6.7	36	1	PSAH_PEA	P20121	pisum sativ
756	2	6.7	36	1	PSAI_ANGLY	P28251	angiopteris
757	2	6.7	36	1	PSAI_BRAOL	Q31909	brassica ol
758	2	6.7	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae

759	2	6.7	36	1	PSAI_CHLVU	P58214	chlorella v
760	2	6.7	36	1	PSAI_CYACA	Q9tm24	cyanidium c
761	2	6.7	36	1	PSAI_GUITH	O78462	guillardia
762	2	6.7	36	1	PSAI_HORVU	P13165	hordeum vul
763	2	6.7	36	1	PSAI_MAIZE	P30980	zea mays (m
764	2	6.7	36	1	PSAI_MARPO	P12185	marchantia
765	2	6.7	36	1	PSAI_MESVI	Q9muq4	mesostigma
766	2	6.7	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
767	2	6.7	36	1	PSAI_ORYSA	P12186	oryza sativ
768	2	6.7	36	1	PSAI_PICAB	O47040	picea abies
769	2	6.7	36	1	PSAI_PORPU	P51387	porphyra pu
770	2	6.7	36	1	PSAI_PSINU	Q8wi10	psilotum nu
771	2	6.7	36	1	PSAI_SKECO	O96813	skeletonema
772	2	6.7	36	1	PSAI_TOBAC	P12187	nicotiana t
773	2	6.7	36	1	PSAI_WHEAT	P25410	triticum ae
774	2	6.7	36	1	PSBI_ARATH	P09970	arabidopsis
775	2	6.7	36	1	PSBI_HORVU	P25876	hordeum vul
776	2	6.7	36	1	PSBI_MARPO	P09969	marchantia
777	2	6.7	36	1	PSBI_ORYSA	P12161	oryza sativ
778	2	6.7	36	1	PSBI_PINTH	P41599	pinus thunb
779	2	6.7	36	1	PSBI_PSEMZ	P29796	pseudotsuga
780	2	6.7	36	1	PSBM_CHLVU	P56325	chlorella v
781	2	6.7	36	1	PSBM_SYNEL	Q8dha7	synechococc
782	2	6.7	36	1	PSBY_ODOSI	P49543	odontella s
783	2	6.7	36	1	PSBY_PORPU	P51206	porphyra pu
784	2	6.7	36	1	PYY_AMICA	P29205	amia calva
785	2	6.7	36	1	PYY_LEPSP	P09473	lepisosteus
786	2	6.7	36	1	PYY_MYOSC	P09641	myoxocephal
787	2	6.7	36	1	PYY_ONCKI	P09474	oncorhynchu
788	2	6.7	36	1	PYY_ORENI	P81028	oreochromis
789	2	6.7	36	1	PYY_PIG	P01305	sus scrofa
790	2	6.7	36	1	PYY_RAJRH	P29206	raja rhina
791	2	6.7	36	1	PYY_RANRI	P29204	rana ridibu
792	2	6.7	36	1	SCK2_CENLL	P45630	centruroide
793	2	6.7	36	1	SCK3_LEIQH	P45660	leiurus qui
794	2	6.7	36	1	SCX1_BUTEU	P15220	buthus eupe
795	2	6.7	36	1	SCXL_LEIQU	P45639	leiurus qui
796	2	6.7	36	1	SPYY_PHYBI	P80952	phyllomedus
797	2	6.7	36	1	TAEK_ACTEQ	P81897	actinia equ
798	2	6.7	36	1	TLN1_CHICK	P54939	gallus gall
799	2	6.7	36	1	TX1B_AGEAP	P15970	agelenopsis
800	2	6.7	36	1	TXAM_METSE	P11495	metridium s
801	2	6.7	36	1	TXD3_PARLU	P83258	paracoelote
802	2	6.7	36	1	TXJB_HADVE	P82226	hadronyche
803	2	6.7	36	1	Y16L_BPT4	P39244	bacterioph
804	2	6.7	36	1	Y297_ARCFU	O29945	archaeoglob
805	2	6.7	36	1	Y4KD_BPCHP	P19188	bacterioph
806	2	6.7	36	1	Y609_BORBU	O51554	borrelia bu
807	2	6.7	36	1	Y619_ARCFU	O29636	archaeoglob
808	2	6.7	36	1	Y699_TREPA	O83697	treponema p
809	2	6.7	36	1	YC12_CYAPA	P48256	cyanophora
810	2	6.7	36	1	YG50_HAEIN	P44281	haemophilus
811	2	6.7	36	1	YRKG_BACSU	P54434	bacillus su
812	2	6.7	37	1	24KD_PLACH	P14592	plasmodium
813	2	6.7	37	1	AFP4_MALPA	P83138	malva parvi
814	2	6.7	37	1	ANP3_PSEAM	P02733	pseudopleur
815	2	6.7	37	1	ATPO_SOLTU	P80504	solanum tub

816	2	6.7	37	1	B2MG_ORENI	Q03423	oreochromis
817	2	6.7	37	1	CAL1_PIG	P30880	sus scrofa
818	2	6.7	37	1	CEC2_MANSE	P14662	manduca sex
819	2	6.7	37	1	CEC3_MANSE	P14663	manduca sex
820	2	6.7	37	1	CEC4_MANSE	P14664	manduca sex
821	2	6.7	37	1	CG2S_LUPAN	P09930	lupinus ang
822	2	6.7	37	1	CS40_STAAU	P81684	staphylococ
823	2	6.7	37	1	CUP4_SARBU	P14486	sarcophaga
824	2	6.7	37	1	DEFA_MYTED	P81610	mytilus edu
825	2	6.7	37	1	ECAA_ECTTU	P49343	ectatomma t
826	2	6.7	37	1	ES2A_RANES	P40845	rana escule
827	2	6.7	37	1	ES2B_RANES	P40846	rana escule
828	2	6.7	37	1	F13A_BOVIN	P12260	bos taurus
829	2	6.7	37	1	GHR3_RAT	P33580	rattus norv
830	2	6.7	37	1	HCYB_CANPG	P83175	cancer pagu
831	2	6.7	37	1	HOXF_RHOOP	P22658	rhodococcus
832	2	6.7	37	1	LPPY_SERMA	P19937	serratia ma
833	2	6.7	37	1	MAUR_PARVE	Q56462	paracoccus
834	2	6.7	37	1	ME20_EUPRA	P26888	euplotes ra
835	2	6.7	37	1	ME22_EUPRA	P58548	euplotes ra
836	2	6.7	37	1	MIBP_PSESP	P04576	pseudomonas
837	2	6.7	37	1	NLT3_VITSX	P80273	vitis sp. (
838	2	6.7	37	1	NLT4_VITSX	P80274	vitis sp. (
839	2	6.7	37	1	NUFM_SOLTU	P80266	solanum tub
840	2	6.7	37	1	OP2A_OXYKI	P83248	oxyopes kit
841	2	6.7	37	1	OP2B_OXYKI	P83249	oxyopes kit
842	2	6.7	37	1	OP2C_OXYKI	P83250	oxyopes kit
843	2	6.7	37	1	OP2D_OXYKI	P83251	oxyopes kit
844	2	6.7	37	1	PETG_ANASP	P58246	anabaena sp
845	2	6.7	37	1	PETG_ANAVA	Q913p7	anabaena va
846	2	6.7	37	1	PETG_ARATH	P56775	arabidopsis
847	2	6.7	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
848	2	6.7	37	1	PETG_CHLEU	P46304	chlamydomon
849	2	6.7	37	1	PETG_CHLRE	Q08362	chlamydomon
850	2	6.7	37	1	PETG_CHLVU	P56305	chlorella v
851	2	6.7	37	1	PETG_CUSRE	P30398	cuscuta ref
852	2	6.7	37	1	PETG_CYAPA	P14236	cyanophora
853	2	6.7	37	1	PETG_EUGGR	P30396	euglena gra
854	2	6.7	37	1	PETG_GUIITH	O78505	guillardia
855	2	6.7	37	1	PETG_MARPO	P12120	marchantia
856	2	6.7	37	1	PETG_MESVI	Q9mun3	mesostigma
857	2	6.7	37	1	PETG_NEPOL	Q9tky8	nephroselmi
858	2	6.7	37	1	PETG_ODOSI	P49470	odontella s
859	2	6.7	37	1	PETG_ORYSA	P12121	oryza sativ
860	2	6.7	37	1	PETG_PINTH	P41614	pinus thunb
861	2	6.7	37	1	PETG_PORPU	P51318	porphyra pu
862	2	6.7	37	1	PETG_PSINU	Q8wi02	psilotum nu
863	2	6.7	37	1	PETG_SKECO	O96811	skeletonema
864	2	6.7	37	1	PETG_SYNEL	Q8dki2	synechococc
865	2	6.7	37	1	PETG_SYNP7	Q9z3g1	synechococc
866	2	6.7	37	1	PIIL_ACHLY	P81720	achromobact
867	2	6.7	37	1	POLN_WEEV	P13896	western equ
868	2	6.7	37	1	PRF1_RAT	P18889	rattus norv
869	2	6.7	37	1	PSAI_ARATH	P56768	arabidopsis
870	2	6.7	37	1	PSAJ_EUGGR	P30394	euglena gra
871	2	6.7	37	1	PSBL_ARATH	P29301	arabidopsis
872	2	6.7	37	1	PSBL_ORYSA	P12166	oryza sativ

873	2	6.7	37	1	PSBM_PINTH	P41608	pinus thunb
874	2	6.7	37	1	PSBY_CYACA	O19893	cyanidium c
875	2	6.7	37	1	PSBY_GUITH	O78433	guillardia
876	2	6.7	37	1	PYY_CHICK	P29203	gallus gall
877	2	6.7	37	1	REV_SIVM2	P08809	simian immu
878	2	6.7	37	1	RK36_ARATH	P12144	arabidopsis
879	2	6.7	37	1	RK36_ASTLO	P24355	astasia lon
880	2	6.7	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
881	2	6.7	37	1	RK36_CHLVU	P56360	chlorella v
882	2	6.7	37	1	RK36_CYACA	Q9tlu9	cyanidium c
883	2	6.7	37	1	RK36_CYAPA	P48131	cyanophora
884	2	6.7	37	1	RK36_EPIVI	P30069	epifagus vi
885	2	6.7	37	1	RK36_EUGGR	P21532	euglena gra
886	2	6.7	37	1	RK36_LOTJA	Q9bbq2	lotus japon
887	2	6.7	37	1	RK36_MARPO	P12142	marchantia
888	2	6.7	37	1	RK36_NEPOL	Q9tl26	nephroselmi
889	2	6.7	37	1	RK36_ODOSI	P49568	odontella s
890	2	6.7	37	1	RK36_OENHO	Q9mtj1	oenothera h
891	2	6.7	37	1	RK36_ORYSA	P12143	oryza sativ
892	2	6.7	37	1	RK36_PEA	P07815	pisum sativ
893	2	6.7	37	1	RK36_PINTH	P41631	pinus thunb
894	2	6.7	37	1	RK36_PORPU	P51296	porphyra pu
895	2	6.7	37	1	RK36_PSINU	Q8why9	psilotum nu
896	2	6.7	37	1	RK36_SPIOL	P12230	spinacia ol
897	2	6.7	37	1	RL36_ANASP	Q8ypk0	anabaena sp
898	2	6.7	37	1	RL36_AQUAE	O66487	aquifex ae
899	2	6.7	37	1	RL36_BACHD	O50631	bacillus ha
900	2	6.7	37	1	RL36_BACST	P07841	bacillus st
901	2	6.7	37	1	RL36_BACSU	P20278	bacillus su
902	2	6.7	37	1	RL36_BORBU	O51452	borrelia bu
903	2	6.7	37	1	RL36_CAMJE	Q9pm84	campylobact
904	2	6.7	37	1	RL36_CLOAB	Q97ek2	clostridium
905	2	6.7	37	1	RL36_CLOPE	Q8xhu7	clostridium
906	2	6.7	37	1	RL36_DEIRA	Q9rsk0	deinococcus
907	2	6.7	37	1	RL36_HAEIN	P46361	haemophilus
908	2	6.7	37	1	RL36_HELPJ	Q9zjt1	helicobacte
909	2	6.7	37	1	RL36_HELPY	P56058	helicobacte
910	2	6.7	37	1	RL36_LEPIN	Q9xd13	leptospira
911	2	6.7	37	1	RL36_LISMO	Q927n0	listeria mo
912	2	6.7	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
913	2	6.7	37	1	RL36_MYCGE	P47420	mycoplasma
914	2	6.7	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
915	2	6.7	37	1	RL36_MYCPN	P52864	mycoplasma
916	2	6.7	37	1	RL36_MYCPU	Q98q05	mycoplasma
917	2	6.7	37	1	RL36_MYCSP	P38015	mycoplasma
918	2	6.7	37	1	RL36_MYCTU	P45810	mycobacteri
919	2	6.7	37	1	RL36_NEIMA	Q9jrb2	neisseria m
920	2	6.7	37	1	RL36_STAAM	Q99s42	staphylococ
921	2	6.7	37	1	RL36_STRCO	O86772	streptomyce
922	2	6.7	37	1	RL36_SYNP6	O24707	synechococc
923	2	6.7	37	1	RL36_THETH	P80256	thermus the
924	2	6.7	37	1	RL36_THETN	Q8r7x8	thermoanaer
925	2	6.7	37	1	RL36_TREPA	O83239	treponema p
926	2	6.7	37	1	RL36_UREPA	Q9pqn7	ureaplasma
927	2	6.7	37	1	RL36_VIBCH	P78001	vibrio chol
928	2	6.7	37	1	RL7_CLOPA	P05393	clostridium
929	2	6.7	37	1	RS15_HELLU	P52820	helix lucor

930	2	6.7	37	1	RUGC_RANRU	P80956	rana rugosa
931	2	6.7	37	1	SCIT_MESTA	P81761	mesobuthus
932	2	6.7	37	1	SCK2_LEIQH	P45628	leiurus qui
933	2	6.7	37	1	SCK3_BUTOC	P59290	buthus occi
934	2	6.7	37	1	SCK3_PARTR	P83112	parabuthus
935	2	6.7	37	1	SCKA_TITSE	P46114	tityus serr
936	2	6.7	37	1	SCKC_LEIQH	P13487	leiurus qui
937	2	6.7	37	1	SMS_PETMA	P21779	petromyzon
938	2	6.7	37	1	TCTP_TRYBB	P35758	trypanosoma
939	2	6.7	37	1	THHS_HORVU	P33045	hordeum vul
940	2	6.7	37	1	TX21_SELHU	P82959	selenocosmi
941	2	6.7	37	1	TX22_SELHU	P82960	selenocosmi
942	2	6.7	37	1	TXD1_PARLU	P83256	paracoelote
943	2	6.7	37	1	TXD2_PARLU	P83257	paracoelote
944	2	6.7	37	1	TXD4_PARLU	P83259	paracoelote
945	2	6.7	37	1	TXJC_HADVE	P82228	hadronyche
946	2	6.7	37	1	TXKB_BUNGR	P29186	bunodosoma
947	2	6.7	37	1	TXOF_HADVE	P81599	hadronyche
948	2	6.7	37	1	TXP3_APTSC	P49268	aptostichus
949	2	6.7	37	1	VA1_BPBF2	P19347	bacterioph
950	2	6.7	37	1	VG40_BPML5	Q05250	mycobacteri
951	2	6.7	37	1	VG65_BPPH2	P16515	bacterioph
952	2	6.7	37	1	VG65_BPPZA	P08384	bacterioph
953	2	6.7	37	1	VGJ_BPPHX	P03651	bacterioph
954	2	6.7	37	1	VP64_NPVBM	P41722	bombyx mori
955	2	6.7	37	1	VPU_HV1Z8	P08807	human immun
956	2	6.7	37	1	Y268_ARCFU	O29971	archaeoglob
957	2	6.7	37	1	Y63_BPT7	P03799	bacterioph
958	2	6.7	37	1	Y692_BORBU	O51635	borrelia bu
959	2	6.7	37	1	Y700_BORBU	O51643	borrelia bu
960	2	6.7	37	1	Y762_BORBU	O51703	borrelia bu
961	2	6.7	37	1	Y846_BORBU	O51786	borrelia bu
962	2	6.7	37	1	YBGT_ECOLI	P56100	escherichia
963	2	6.7	37	1	YC12_CHLVU	P56328	chlorella v
964	2	6.7	37	1	YDA3_SCHPO	Q10345	schizosacch
965	2	6.7	37	1	YIM4_BPPH1	P10428	bacterioph
966	2	6.7	37	1	YQGE_BACCA	P28753	bacillus ca
967	2	6.7	37	1	YRYL_CAEEL	Q19177	caenorhabdi
968	2	6.7	38	1	AFP5_MALPA	P83139	malva parvi
969	2	6.7	38	1	BD01_BOVIN	P46159	bos taurus
970	2	6.7	38	1	BD08_BOVIN	P46166	bos taurus
971	2	6.7	38	1	COA3_XANCP	Q07484	xanthomonas
972	2	6.7	38	1	CRS3_NOTGO	P15534	nototodarus
973	2	6.7	38	1	CU47_LACCU	P80323	lactobacill
974	2	6.7	38	1	DCHS_MICSP	P00863	micrococcus
975	2	6.7	38	1	DEF4_LEIQH	P41965	leiurus qui
976	2	6.7	38	1	DEF7_SPIOL	P81573	spinacia ol
977	2	6.7	38	1	DEF1_AESCY	P80154	aeschna cya
978	2	6.7	38	1	DEF1_MYTGA	P80571	mytilus gal
979	2	6.7	38	1	DLP3_ORNAN	P82141	ornithorhyn
980	2	6.7	38	1	DPOB_BOVIN	Q27958	bos taurus
981	2	6.7	38	1	E2F1_RAT	O09139	rattus norv
982	2	6.7	38	1	EST5_DROMO	P10095	drosophila
983	2	6.7	38	1	EXE1_HELNU	P04203	heloderma s
984	2	6.7	38	1	FER_METPR	P81542	metallospha
985	2	6.7	38	1	GLUM_HYDCO	P23063	hydrolagus
986	2	6.7	38	1	GME1_RAT	Q9quz8	rattus norv

987	2	6.7	38	1	H5_COLLI	P02260	columba liv
988	2	6.7	38	1	HIS1_MACFA	P34084	macaca fasc
989	2	6.7	38	1	HMG2_BOVIN	P40673	bos taurus
990	2	6.7	38	1	HOXH_RHOOP	P22661	rhodococcus
991	2	6.7	38	1	ID5B_ADEPA	P09942	adenanthera
992	2	6.7	38	1	ID5B_PROJU	P32734	prosopsis j
993	2	6.7	38	1	MFA2_YEAST	P34166	saccharomyc
994	2	6.7	38	1	MUTS_YEREN	P47763	yersinia en
995	2	6.7	38	1	PA21_MATBI	P24644	maticora bi
996	2	6.7	38	1	PA22_MATBI	P24645	maticora bi
997	2	6.7	38	1	PACA_URAJA	P81039	uranoscopu
998	2	6.7	38	1	PERE_PIG	P80550	sus scrofa
999	2	6.7	38	1	PETG_SYNY3	P74149	synechocyst
1000	2	6.7	38	1	POI_MUSDO	P81765	musca domes

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.

AC P81175;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Fatty acid-binding protein, intestinal (I-FABP) (FABP1) (Fragments).

OS Rhamdia sapo.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Pimelodidae; Rhamdia.

OX NCBI_TaxID=55673;

RN [1]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=98036128; PubMed=9370361;

RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,

RA Santome J.A.;

RT "Amino acid sequence, binding properties and evolutionary

RT relationships of the basic liver fatty-acid-binding protein from the

RT catfish Rhamdia sapo.";

RL Eur. J. Biochem. 249:510-517(1997).

CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: INTESTINE.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

DR InterPro; IPR000463; Fatty_acid_BP.

DR PROSITE; PS00214; FABP; PARTIAL.

KW Transport; Lipid-binding.

FT NON_TER 1 1

FT NON_CONS 12 13

FT NON_CONS 20 21

FT NON_CONS 28 29

FT NON_TER 33 33

SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 16.7%; Score 5; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 13 SVSEI 17

RESULT 2

DMD_RAT

ID DMD_RAT STANDARD; PRT; 29 AA.
AC P11530;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dystrophin (Fragment).
GN DMD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122671; PubMed=3340214;
RA Nudel U., Robzyk K., Yaffe D.;
RT "Expression of the putative Duchenne muscular dystrophy gene in
RT differentiated myogenic cell cultures and in the brain.";
RL Nature 331:635-638(1988).
CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the
CC plasma membrane.
CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1
CC and SNTG2 (By similarity).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07000; CAA30057.1; -.
DR PIR; S01614; S01614.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR PROSITE; PS00019; ACTININ_1; PARTIAL.
DR PROSITE; PS00020; ACTININ_2; PARTIAL.
DR PROSITE; PS01159; WW_DOMAIN_1; PARTIAL.
DR PROSITE; PS50020; WW_DOMAIN_2; PARTIAL.
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
KW Repeat.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 13.3%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 3

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.
AC P08377;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sarcotoxin IC.
OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7386;
RN [1]
RP SEQUENCE.
RX MEDLINE=85207747; PubMed=3888997;
RA Okada M., Natori S.;
RT "Primary structure of sarcotoxin I, an antibacterial protein induced
RT in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.";
RL J. Biol. Chem. 260:7174-7177(1985).
CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH
CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
DR PIR; C22625; CKFHCS.
DR InterPro; IPR000875; Cecropin.
DR InterPro; IPR003253; Sarctxn_cecrpn.
DR Pfam; PF00272; cecropin; 1.
DR ProDom; PD001670; Sarctxn_cecrpn; 1.
DR PROSITE; PS00268; CECROPIN; 1.
KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
FT MOD_RES 39 39 AMIDATION.
SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 13.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 2 WLRK 5

RESULT 4

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.
AC P80673;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
 GN GROL OR GROEL OR MOPA.
 OS Mycobacterium smegmatis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved Mycobacterium smegmatis.";
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.
 DR InterPro; IPR001844; Chaprnin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 18 LNS 20

RESULT 5

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
 AC P80499;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=97077345; PubMed=8919912;

RA Jansch L., Krufft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria.";
 RL Plant J. 9:357-368(1996).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
 DR InterPro; IPR002124; COX5B.
 DR PROSITE; PS00848; COX5B; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
 |||
 Db 2 VSE 4

RESULT 6

GUN_SCHCO

ID GUN_SCHCO STANDARD; PRT; 28 AA.
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;
 RT "Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases.";
 RL FEBS Lett. 414:359-361(1997).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 KW Lipoprotein.
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 7 EWL 9

RESULT 7

PA23_TRIST

ID PA23_TRIST STANDARD; PRT; 28 AA.
AC P82894;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic 3 (EC 3.1.1.4) (PA2-III) (PLA2-III)
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).
OS Trimeresurus stejnegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=39682;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Li S.Y., Wang W.Y., Xiong Y.L.;
RT "Isolation, sequence and characterization of five variants of
RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides. Hemolytic and neurotoxic
CC activities are not detected.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
CC SUBFAMILY.
DR HSSP; P82287; 1QLL.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3023 MW; 042104521CA1F103 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||
Db 5 LGK 7

RESULT 8

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.

AC P20260;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine 2-acylhydrolase) (Fragment).

OS Pseudechis porphyriacus (Red-bellied black snake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Acanthophiinae; Pseudechis.

OX NCBI_TaxID=8671;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=89388835; PubMed=2675391;

RA Schmidt J.J., Middlebrook J.L.;

RT "Purification, sequencing and characterization of pseudexin

phospholipases A2 from Pseudechis porphyriacus (Australian

red-bellied black snake).";

RL Toxicon 27:805-818(1989).

CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.

CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-

CC acylglycerophosphocholine + a fatty acid anion.

CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I

CC SUBFAMILY.

DR PIR; C32416; C32416.

DR HSSP; P00592; 2PHI.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; phoslip; 1.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR PROSITE; PS00119; PA2_ASP; PARTIAL.

DR PROSITE; PS00118; PA2_HIS; PARTIAL.

KW Hydrolase; Lipid degradation; Calcium; Multigene family.

FT NON_TER 28 28

SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAA0D5 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQL 7

|||

Db 3 IQL 5

RESULT 9

VI03_VACCP

ID VI03_VACCP STANDARD; PRT; 28 AA.

AC Q00334;

DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Protein I3 (Fragment).
 GN I3L.
 OS Vaccinia virus (strain L-IVP).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=31531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91066899; PubMed=2250685;
 RA Ryazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,
 RA Mikryukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,
 RA Malygin E.G.;
 RT "Molecular-biological study of vaccinia virus genome. II.
 RT Localization and nucleotide sequence of vaccinia virus genes coding
 RT for proteins 36K and 12K.";
 RL Mol. Biol. (Mosk) 24:968-976(1990).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
 CC THE LATE PHASE OF INFECTION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X61165; CAA43473.1; -.
 DR InterPro; IPR006754; Pox_I3.
 DR Pfam; PF04661; Pox_I3; 1.
 KW Early protein; Late protein.
 FT NON_TER 1 1
 SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12
 |||
 Db 5 NLG 7

RESULT 10

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.
 AC P48142; P01285;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 11

VIP_RANRI
 ID VIP_RANRI STANDARD; PRT; 28 AA.
 AC P81016;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 12

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.

AC P04565;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Vasoactive intestinal peptide (VIP).

GN VIP.

OS Ovis aries (Sheep),

OS Capra hircus (Goat), and

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940, 9925, 9615;

RN [1]

RP SEQUENCE.

RC SPECIES=Sheep; TISSUE=Brain;

RX MEDLINE=91045331; PubMed=2235680;

RA Gafvelin G.;

RT "Isolation and primary structure of VIP from sheep brain.";

RL Peptides 11:703-706(1990).

RN [2]

RP SEQUENCE.

RC SPECIES=Sheep; TISSUE=Small intestine;

RX MEDLINE=91239834; PubMed=2034821;

RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,

RA Christophe J.;

RT "Purification and amino acid sequence of vasoactive intestinal

peptide, peptide histidine isoleucinamide and secretin from the ovine
 small intestine.";

RL Regul. Pept. 32:169-179(1991).

RN [3]

RP SEQUENCE.

RC SPECIES=C.hircus, and C.familiaris;

RX MEDLINE=86313167; PubMed=3748846;

RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;

RT "Purification and amino acid sequences of dog, goat and guinea pig

VIPs.";

RL Peptides 7 Suppl. 1:17-20(1986).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60304; A60304.
 DR PIR; B60072; VRSH.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 10.0%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 13

GALA_ALLMI

ID GALA_ALLMI STANDARD; PRT; 29 AA.
 AC P47215;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95023390; PubMed=7524049;
 RA Wang Y., Conlon J.M.;
 RT "Purification and primary structure of galanin from the alligator
 RT stomach."
 RL Peptides 15:603-606(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.

FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 14

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
AC P47214;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.
OX NCBI_TaxID=7924;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95083480; PubMed=7527531;
RA Wang Y., Conlon J.M.;
RT "Purification and characterization of galanin from the
RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
RT (*Scyliorhinus canicula*).";
RL Peptides 15:981-986(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 15

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
 AC P30802;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 16

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
 AC P47213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95164756; PubMed=7532194;
 RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
 RT "Characterization of trout galanin and its distribution in trout
 RT brain and pituitary.";
 RL J. Comp. Neurol. 350:63-74(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 17

GALA_RANRI

ID GALA_RANRI STANDARD; PRT; 29 AA.
 AC P47216;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 18

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
 AC P31234;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN OR GLNN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92158824; PubMed=1724081;
 RA Sillard R., Langel U., Joernvall H.;
 RT "Isolation and characterization of galanin from sheep brain.";
 RL Peptides 12:855-859(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 19

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.
AC P31297;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon.
GN GCG.
OS Chinchilla brevicaudata (Chinchilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
OC Chinchilla.
OX NCBI_TaxID=10152;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045327; PubMed=2235678;
RA Eng J., Kleinman W.A., Chu L.S.;
RT "Purification of peptide hormones from chinchilla pancreas by
RT chemical assay.";
RL Peptides 11:683-685(1990).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A60413; GCCB.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone.
SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15
|||
Db 12 KHL 14

RESULT 20

IPYR_DESVH

ID IPYR_DESVH STANDARD; PRT; 29 AA.
AC P19371;
DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase) (Fragment).
 OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin
 RT and a new, highly active, enzyme."
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).
 CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEI 5
 |||
 Db 15 SEI 17

RESULT 21

NUO1_SOLTU

ID NUO1_SOLTU STANDARD; PRT; 29 AA.
 AC P80267;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,

RA Grohmann L. ;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of
 RT Solanum tuberosum." ;
 RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 DR PIR; I49732; I49732.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKK 27
 |||
 Db 2 RKK 4

RESULT 22

P2SM_LOXIN

ID P2SM_LOXIN STANDARD; PRT; 29 AA.
 AC P83046;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sphingomyelinase P2 (EC 3.1.4.12) (Fragment).
 OS Loxosceles intermedia (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
 OX NCBI_TaxID=58218;
 RN [1]
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBCELLULAR
 RP LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Venom;
 RX MEDLINE=99009277; PubMed=9790962;
 RA Tambourgi D.V., Magnoli F.C., van den Berg C.W., Morgan B.P.,
 RA de Araujo P.S., Alves E.W., Da Silva W.D.;
 RT "Sphingomyelinases in the venom of the spider Loxosceles intermedia
 RT are responsible for both dermonecrosis and complement-dependent
 RT hemolysis." ;
 RL Biochem. Biophys. Res. Commun. 251:366-373(1998).
 CC -!- FUNCTION: Has sphingomyelinase activity. Induces complement-
 CC dependent hemolysis and dermonecrosis.
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +
 CC choline phosphate.
 CC -!- COFACTOR: Calcium ion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

KW Hydrolase; Toxin; Calcium; Hemolysis.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3281 MW; 4488EDD619BD2398 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12
|||
Db 25 NLG 27

RESULT 23

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii."
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
|||
Db 11 EWL 13

RESULT 24

RS7_METTE

ID RS7_METTE STANDARD; PRT; 29 AA.
AC O93639;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7P (Fragment).
 GN RPS7P OR S7.
 OS Methanosarcina thermophila.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=99059471; PubMed=9845338;
 RA Thomas T., Cavicchioli R.;
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
 RT thermophilic methanogens.";
 RL FEBS Lett. 439:281-287(1998).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF026165; AAC79199.1; -.
 DR PIR; T44245; T44245.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 22 ERV 24

RESULT 25

SODC_OLEEU

ID SODC_OLEEU STANDARD; PRT; 29 AA.
 AC P80740;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e

DE V) (Fragment).
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea.";
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro; IPR001424; SOD_CU_ZN.
 DR Pfam; PF00080; sodcu; 1.
 DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
 KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 7 LNS 9

RESULT 26

TL16_SPIOL

ID TL16_SPIOL STANDARD; PRT; 29 AA.
 AC P81834;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=98175931; PubMed=9506969;
 RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;
 RT "The thylakoid lumen of chloroplasts. Isolation and
 RT characterization.";

RL J. Biol. Chem. 273:6710-6716(1998).
CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 27

DMS3_PHYSA
ID DMS3_PHYSA STANDARD; PRT; 30 AA.
AC P80279;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 3 (DS III).
OS Phyllomedusa sauvagei (Sauvage's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8395;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=94139686; PubMed=8306981;
RA Mor A., Nicolas P.;
RT "Isolation and structure of novel defensive peptides from frog skin.";
RL Eur. J. Biochem. 219:145-154(1994).
CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 23 KKL 25

RESULT 28

FTN_BACFR
ID FTN_BACFR STANDARD; PRT; 30 AA.

AC P28733;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ferritin like protein (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=20656-2-1;
 RX MEDLINE=92406001; PubMed=1526453;
 RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;
 RT "Isolation of a ferritin from Bacteroides fragilis.";
 RL FEMS Microbiol. Lett. 74:207-212(1992).
 CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF
 CC OXYGEN.
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT
 CC 17 kDa).
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.
 DR PROSITE; PS50905; FERRITIN_LIKE; 1.
 KW Iron storage; Iron; Metal-binding.
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.
 FT METAL 17 17 IRON (BY SIMILARITY).
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQ 29
 |||
 Db 5 KLQ 7

RESULT 29

GLUM_ANGAN

ID GLUM_ANGAN STANDARD; PRT; 30 AA.
 AC P41521;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glucagon-like peptide (GLP).
 OS Anguilla anguilla (European freshwater eel), and
 OS Anguilla rostrata (American eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7936, 7938;
 RN [1]
 RP SEQUENCE.

RC SPECIES=A.anguilla, and A.rostrata;
 RC TISSUE=Pancreas;
 RX MEDLINE=91340068; PubMed=1874385;
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;
 RT "The primary structure of glucagon-like peptide but not insulin has
 RT been conserved between the American eel, *Anguilla rostrata* and the
 RT European eel, *Anguilla anguilla*.";
 RL Gen. Comp. Endocrinol. 82:23-32(1991).
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; B61125; B61125.
 DR PIR; C61125; C61125.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation.
 FT MOD_RES 30 30 AMIDATION.
 SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30
 |||
 Db 14 LQD 16

RESULT 30
 OTCC_AERPU
 ID OTCC_AERPU STANDARD; PRT; 30 AA.
 AC P11726;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)
 DE (Fragment).
 OS *Aeromonas punctata* (*Aeromonas caviae*).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; *Aeromonas*.
 OX NCBI_TaxID=648;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIB 9232;
 RX MEDLINE=85104799; PubMed=3968036;
 RA Falmagne P., Portetelle D., Stalon V.;
 RT "Immunological and structural relatedness of catabolic ornithine
 RT carbamoyltransferases and the anabolic enzymes of enterobacteria.";
 RL J. Bacteriol. 161:714-719(1985).
 CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
 CC + L-citrulline.
 CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 DR InterPro; IPR006130; Asp/Orn_Cotranf.
 DR InterPro; IPR006132; OTCace_P.

DR Pfam; PF02729; OTCace_N; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW Transferase; Arginine metabolism.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6
|||
Db 19 EIQ 21

RESULT 31

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.
AC P82415;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G2.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii."
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 32

PCG3_PACGO

ID PCG3_PACGO STANDARD; PRT; 30 AA.

AC P82416;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ponericin G3.
 OS Pachycondyla goeldii (Ponerine ant).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Ponerinae; Pachycondyla.
 OX NCBI_TaxID=118888;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Venom;
 RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant Pachycondyla goeldii.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

 Query Match 10.0%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
 |||
 Db 11 EWL 13

RESULT 33
 PSAM_PORPU
 ID PSAM_PORPU STANDARD; PRT; 30 AA.
 AC P51395;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Photosystem I reaction centre subunit XII (PSI-M).
 GN PSAM.
 OS Porphyra purpurea.
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TaxID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RA Reith M.E., Munholland J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
 RT genome.";
 RL Plant Mol. Biol. Rep. 13:333-335(1995).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U38804; AAC08281.1; -.
DR PIR; S73316; S73316.
KW Photosystem I; Photosynthesis; Chloroplast.
SQ SEQUENCE 30 AA; 3338 MW; 8D1930479D8A5527 CRC64;

```

```

Query Match          10.0%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 LGK 13
        |||
Db      24 LGK 26

```

RESULT 34

```

TX2_THRPR
ID TX2_THRPR          STANDARD;          PRT;          30 AA.
AC P83476;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toxin ProTx-II.
OS Thrixopelma pruriens (Green velvet).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Theraphosidae; Thrixopelma.
OX NCBI_TaxID=213387;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
RP SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=22363233; PubMed=12475222;
RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,
RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,
RA Mehl J.T., Cohen C.J., Smith M.M.;
RT "Two tarantula peptides inhibit activation of multiple sodium
RT channels.";
RL Biochemistry 41:14734-14747(2002).
CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.
CC Shifts the voltage-dependence of channel activation to more
CC positive potentials.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.
CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
CC TOXIN FAMILY.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;
KW Sodium channel inhibitor.

```

FT DISULFID 2 16
FT DISULFID 9 21
FT DISULFID 15 25
SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 27 KKL 29

RESULT 35

UP61_UPEIN

ID UP61_UPEIN STANDARD; PRT; 30 AA.
AC P82037;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 6.1.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: UNKNOWN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.
KW Amphibian defense peptide.
SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 36

UP62_UPEIN

ID UP62_UPEIN STANDARD; PRT; 30 AA.
AC P82038;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 6.2.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata."
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: UNKNOWN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.
 KW Amphibian defense peptide.
 SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
 |||
 Db 24 KKL 26

RESULT 37

VAA2_EQUAR

ID VAA2_EQUAR STANDARD; PRT; 30 AA.
 AC Q04238;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)
 DE (Fragment).
 OS Equisetum arvense (Field horsetail) (Common horsetail).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
 OX NCBI_TaxID=3258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93138084; PubMed=8422915;
 RA Starke T., Gogarten J.P.;
 RT "A conserved intron in the V-ATPase A subunit genes of plants and
 RT algae."
 RL FEBS Lett. 315:252-258(1993).
 CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF
 CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
 CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
 CC CELLS.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).

CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
 CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
 CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
 CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
 CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa
 CC V-ATPASE SUBUNIT IN PSILLOTUM AND EQUISETUM.
 CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X56984; CAA40302.1; -.
 DR PIR; S21815; S21815.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
 KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
 KW Multigene family.
 FT NON_TER 1 1
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MER 20
 |||
 Db 23 MER 25

RESULT 38
 Y523_BORBU
 ID Y523_BORBU STANDARD; PRT; 30 AA.
 AC O51473;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein BB0523.
 GN BB0523.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,

RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia*
RT burgdorferi.";
RL Nature 390:580-586(1997).

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AE001154; AAC66894.1; -.
DR PIR; B70165; B70165.
DR TIGR; BB0523; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 30 AA; 3431 MW; DE437B15D2A48AA8 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
|||
Db 26 ERV 28

RESULT 39

CEC1_PIG

ID CEC1_PIG STANDARD; PRT; 31 AA.
AC P14661;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cecropin P1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=90083227; PubMed=2512577;
RA Lee J.-Y., Boman A., Chuanxin S., Andersson M., Joernvall H., Mutt V.,
RA Boman H.G.;
RT "Antibacterial peptides from pig intestine: isolation of a mammalian
RT cecropin.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9159-9162(1989).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=93011123; PubMed=1396696;
RA Sipos D., Andersson M., Ehrenberg A.;
RT "The structure of the mammalian antibacterial peptide cecropin P1 in
RT solution, determined by proton-NMR.";
RL Eur. J. Biochem. 209:163-169(1992).
CC !- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST

CC SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. ACTS BY A
 CC NONPORE MECHANISM.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
 DR PIR; A36221; A36221.
 DR InterPro; IPR000875; Cecropin.
 DR Pfam; PF00272; cecropin; 1.
 DR PROSITE; PS00268; CECROPIN; 1.
 KW Antibiotic.
 SQ SEQUENCE 31 AA; 3339 MW; CB2B374A8B153850 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
 |||
 Db 8 KKL 10

RESULT 40

CXMA_CONMR

ID CXMA_CONMR STANDARD; PRT; 31 AA.
 AC P56708;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mu-O-conotoxin MrVIA.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RX MEDLINE=95348106; PubMed=7622492;
 RA McIntosh J.M., Hasson A., Spira M.E., Gray W.R., Li W., Marsh M.,
 RA Hillyard D.R., Olivera B.M.;
 RT "A new family of conotoxins that blocks voltage-gated sodium
 RT channels.";
 RL J. Biol. Chem. 270:16796-16802(1995).
 CC -!- FUNCTION: Mu-O-conotoxins bind and block voltage-sensitive sodium
 CC channel (VSSC).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=3487.8; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. MU-O-TYPE
 CC FAMILY.
 DR PIR; A58586; A58586.
 KW Toxin; Sodium channel inhibitor.
 FT DISULFID 2 20 BY SIMILARITY.
 FT DISULFID 9 25 BY SIMILARITY.
 FT DISULFID 19 30 BY SIMILARITY.
 SQ SEQUENCE 31 AA; 3495 MW; 741FA610E6F9D289 CRC64;

Query Match 10.0%; Score 3; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 3 RKK 5

Search completed: January 14, 2004, 10:35:36
Job time : 5.95327 secs